

SEQUENCE LISTING

10/573600

<110> The Trustees of the University of Pennsylvania
 Wilson, James M.
 Gao, Guangping
 Alvira, Mauricio R.
 Vandenbergh, Luk H.

<120> Adeno-Associated Virus (AAV) Clades, Sequences, Vectors
 Containing Same, and Uses Therefor

10/573600
 2005 MAR 2005

<130> UPN-P3230PCT

<150> US 60/508,226

<151> 2003-09-30

<150> US 60/566,546

<151> 2004-04-29

<160> 236

<170> PatentIn version 3.3

<210> 1

<211> 2211

<212> DNA

<213> adeno-associated virus, clone hu.31

<400> 1
 atggctgccc atgggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60
 gagtggtggg ctttgaaacc tggagcccct caaccaagg caaatcaaca acatcaagac 120
 aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cgactcgac 180
 aagggggagc cggtaacagc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aggccggaga caaccggtac ctcaagtaca accacgccga cgccgagttc 300
 caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttcag 360
 gccaaaaaga ggcttcttga acctcttggg ctggttgagg aagcggctaa gacggctcct 420
 ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggatttggc 480
 aaatcgggtg cacagcccgc taaaagaga ctcaatttcg gtcagactgg cgacacagag 540
 tcagtcccag acctcaacc aatcggagaa cctcccgag cccctcagg tgtgggatct 600
 cttacaatgg cttcaggtgg tggcgacca gtggcagaca ataacgaagg tgccgatgga 660
 gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaattc 780
 tccaacagca catctggagg atcttcaa atgacaagcct acttcggcta cagaccccc 840
 tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900
 ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960
 cagggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa cttaccagc 1020
 acgggtccagg tcttcacgga ctcaactat cagctccgt acgtgctcgg gtcggctcac 1080
 gagggctgcc tcccgcggtt cccagcggac gttttcatga ttctcagta cgggtatctg 1140
 acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200
 ccgtcgcaaa tgctaagaac gggtaacaac ttccagtcca gctacgagtt tgagaacgta 1260
 cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320
 gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaacg 1380
 ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggagaaa ctacatacct 1440
 ggaccagct accgacaaca acgtgtctca accactgtga ctcaaaca caacagcgaa 1500
 tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560
 ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttcctt gtctggatct 1620
 ttaatttttg gcaacaagg aactggaaga gacaacgtgg atgaggacaa agtcatgata 1680
 accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740
 gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800
 atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggccc 1860

aaaattcctc	acacggacgg	caactttcac	ccttctccgc	tgatgggagg	gtttggaatg	1920
aagcaccgcg	ctcctcagat	cctcatcaaa	aacacacctg	tacctgcgga	tcctccaacg	1980
gccttcaaca	aggacaagct	gaactctttc	atcacccagt	attctactgg	ccaagtcagc	2040
gtggagatcg	agtgggagct	gcagaaggaa	aacagcaagc	gctggaaccc	ggagatccag	2100
tacacttcca	actattacaa	gtctaataat	gttgaatttg	ctgttaatac	tgaagggtga	2160
tatagtgaac	cccgcccat	tggcaccaga	tacctgactc	gtaatctgta	a	2211

<210> 2
 <211> 2211
 <212> DNA
 <213> new AAV serotype, clone hu.32

<400> 2		
atggctgccc	atggttatct	tccagattgg
cagtgtgga	agctcaaac	tgccccacca
gacagcagg	gtcttggtc	tcctgggtac
aagggggagc	cggtaacgc	agcagacgcg
cagcagctca	aggccggaga	caaccctgac
caggagcggc	tcaaagaaga	tacgtctttt
gccaaaaaga	ggcttcttga	acctcttgg
ggaaagaaga	ggcctgtaga	gcagctctct
aaatcgggtt	cacagccgc	taaaaagaaa
tcagtccccg	acctcaacc	aatcggagaa
cttacaatgg	cttcaggtgg	tggcgcacca
gtgggtagtt	cctcgggaaa	ttggcattgc
accaccagca	cccgaacctg	ggccctgccc
tccaacagca	catctggagg	atcttcaaat
tggggggtatt	ttgacttcaa	cagattccac
ctcatcaaca	acaactgggg	attccggcct
caggtcaaag	aggttacgga	caacaatgga
acggtccagg	tccttcacgga	ctcagactat
gagggctgcc	tcccgcggtt	cccagcggac
acgcttaatg	atgggagcca	ggccgtgggt
ccgtcgcaaa	tgctaagaac	gggtaacaac
cctttccata	gcagctacgc	tcacagccaa
gaccaatact	tgtactatct	ctcaaagact
ctaaaattca	gcgtggccgg	accagcaaac
ggaccagct	accgacaaca	acgtgtctca
tttgcttggc	ctggagcttc	ttcttgggct
ggacctgcta	tggccagcca	caaagaagga
ttaatttttg	gcaacaagga	aactggaaga
accaacgaag	aagaaattaa	aactactaac
gccacaaacc	accagagtgc	ccaagcacag
atacttccgg	gtatggtttg	gcaggacaga
aaaattcctc	acacggacgg	caactttcac
aagcaccgcg	ctcctcagat	cctcatcaaa
gccttcaata	aggacaagct	gaactctttc
gtggagattg	agtgggagct	gcagaaggaa
tacacttcca	actattacaa	gtctaataat
		gttgaatttg
		ctgttaatac
		tgaagggtga
		2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 3
 <211> 2211
 <212> DNA
 <213> adeno-associated virus, human clone 9

<400> 3
 atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60
 gagtggtggg ctttgaaacc tggagcccct caaccgaagg caaatcaaca acatcaagac 120
 aacgctcgag gtcttggtct tccgggttac aaataccttg gaccgcgcaa cggactcgac 180
 aagggggagc cggtaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aggcgggaga caaccgtac ctcaagtaca accacgccga cgcgagttc 300
 caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag 360
 gccaaaaaga ggcttcttga acctcttggg ctggttgagg aagcggctaa gacggctcct 420
 ggaaagaaga ggcctgtaga gcagtctctt caggaaccgg actcctccgc gggattggc 480
 aaatcgggtg cacagcccgc taaaagaga ctcaatttcg gtcagactgg cgacacagag 540
 tcagtcccag acctcaacc aatcggagaa cctcccgcag cccctcagg tgtgggatct 600
 cttacaatgg cttcaggtgg tggcgacca gtggcagaca ataacgaagg tgccgatgga 660
 gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaacc 780
 tccaacagca catctggagg atcttcaa atgacaacgcct acttcggcta cagaccccc 840
 tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900
 ctcacacaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960
 cagggtcaaag aggttacgga caacaatgga gtcaagacca tcgccataaa ccttaccagc 1020
 acggtccagg tcttcacgga ctacagactat cagctcccgt acgtgctcgg gtcggctcac 1080
 gagggctgcc tcccgcggtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140
 acgcttaatg atggaagcca ggccgtgggt cgctcgtcct tttactgcct ggaatatttc 1200
 ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260
 cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320
 gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380
 ctaaaattca gtgtggcccg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440
 ggaccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500
 tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560
 ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620
 ttaatttttg gcaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680
 accaacgaag aagaatttaa aactactaac ccggtagcaa cggagtccta tggacaagt 1740
 gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800
 atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860
 aaaattcctc acacggacgg caactttcac cttctccgc tgatgggagg gtttggaatg 1920
 aagcaccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980
 gccttcaaca aggacaagct gaactctttc atcaccaggt attctactgg ccaagtcagc 2040
 gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100
 tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160
 tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 4
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone hu.17

<400> 4
 atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

```

gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctggtgct tcctggctgc aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcgtt ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcattc 480
ggcaagacag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540
gagtcaagtgc ccgacctca accaatcgga gaacccccg caggccctc tggctctggga 600
tctgtataca tggctgcagg cgggtggcgtt ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcttcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gacccgaac ctgggccctc cccacctaca acaaccact ctacaagcaa 780
atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt taacagattc cactgccact tctcaccag tgactggcag 900
cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960
atccaggta aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgag 1080
caccagggtc gcccgctcc gttcccgccg gacgtcttca tgattctca gtacgggtac 1140
ctgactctga acaacggcag tcaggccgtg ggccgttctt ctttctactg cctggagtac 1200
tttcttctc aaatgcggag aacgggcaac aactttgagt tcagctacca gtttgaggac 1260
gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaacccccctc 1320
atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtag cgcaggaaact 1380
cagcagttgc tattttctca ggccggcctt aataacatgt cggctcaggc caaaaactgg 1440
ctaccggggc cctgttaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500
agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560
aatcccgggt tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620
ggagtcttga tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680
atgctaacca gtgaggaaga aatcaaaacc accaaccagc tggccacaga acagtacggc 1740
gtggtggccg ataacctgca acagcaaaac gccgtccta ttgtaggggc cgtcaacagt 1800
caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatc 1860
tgggccaaga ttcttcacac ggacggcaac ttctatcctt cgccgtgat gggaggcttt 1920
ggactgaaac acccgctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980
ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040
gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgtg gaaccagag 2100
attcagtata cttccaacta taacaaatct gttaatgtgg actttactgt ggacactaat 2160
ggtgtgtatt cagagcctcg cccattggc accagatacc tgactcgtaa tctgtaa 2217

```

```

<210> 5
<211> 2217
<212> DNA
<213> new AAV serotype, clone hu.6

```

```

<400> 5
atggctgccg atggttatct tccagattgg ctgcaggaca acctctctga gggcattcgc 60
gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

```



```

gccaaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccatcacc cagcgttctc cagactcctc tacgggcatc 480
ggcaagacag gccagcagcc cgcaaaaag agactcaact ttgggcagac tggcgactca 540
gagtcagtgc ccgacctca accaatcgga gaacccccg caggccctc tggctctgga 600
tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcctcagg aaattggcat tgcgattccg catggctggg cgacagagtc 720
atcaccacca gcaccgacc ctgggcccctc cccacctaca acaaccacct ctacaagcaa 780
atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960
atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080
caccagggct gcccgctcc gttcccgcg gacgtcttca tgattcctca gtacgggtac 1140
ctgactctga acaacggcag tcaggccgtg ggccgttctc ctttctactg cctggagtac 1200
tttcttctc aaatgcggag aacgggcaac aactttgagt tcagctacca gtttgaggac 1260
gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaacccccctc 1320
atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380
cagcagttgc tattttctca ggccgggcct aataacatgt cggctcaggc caaaaactgg 1440
ctaccgggc cctgtaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500
agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560
aatcccgtg tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620
ggagtcttga tgtttgagg aaaggagct ggaaaagaca acgtggacta tagcagcggt 1680
atgctaacca gtgaggaaga aatcaaaacc accaaccagc tggccacaga acagtacggc 1740
gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaacagt 1800
caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatc 1860
tgggccaaga ttcctcacac ggacggcaac tttcatcctt cgccgctgat gggaggcttt 1920
ggactgaaac acccgctcc tcagatcctg attaagaata cactgttcc cgcgatcct 1980
ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040
gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgtg gaaccagag 2100
attcagtata ctccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160
ggtacttatt cagagcctcg cccattggc acccgttacc tcaccgtaa cctgtaa 2217

```

```

<210> 6
<211> 2217
<212> DNA
<213> new AAV serotype, clone hu.41

```

```

<400> 6
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggagg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctgggtgt tcctggctac aagtacctg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctc agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagaagc gggttctcga acctctcggg ccggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgccacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggctctgga 600
tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660

```

```

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
atccagggtca aggaggtcac gcagaatgaa ggcaccaaga ccgtcgcaa taaccttacc 1020
agcacgattc aggtattttac ggactcggaa taccagctgc cgtacgtcct cggtcccgcg 1080
caccagggtc gcctgcctcc gttcccgcg gacgtcttca tgattccca gtacggctac 1140
cttacctga acaatggaag tcaagccgta ggccgttctt ctttctactg cctggaatat 1200
tttccatctc aaatgctcgc aactggaaac aattttgaat tcagctacac cttcgaggac 1260
gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatccttc 1320
atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaaac tcaagggtacc 1380
cagcaattgt tattttctca agctgggctt gcaaacatgt cggtcaggc taagaactgg 1440
ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500
agcaactttg cttggactgg tgccaccaa tatcacctga acggaagaga ctctttggta 1560
aatcccgggt tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcgagt 1620
ggagtctctga tgtttgaaa acaggggtgtt ggaagagaca atgtggacta cagcagcgtt 1680
atgctaacca gcgaagaaga aattaaaacc actaaccttg tagccacaga acaatacgggt 1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca ggtcccatc 1860
tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaata gggaggattt 1920
ggactgaagc acccacttcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980
ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaactgtg gaaccagag 2100
attcagtaca cttcaaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
ggaacttatt ctgagcctcg cccattgggt actcgttacc tcaccgtaa tctgtaa 2217

```

```

<210> 7
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.38

```

```

<400> 7
atggctgctg acggttatct tccagattgg ctgcaggaca acctctctga gggcattcgc 60
gagtgggtgg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgaaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc caccggcatc 480
ggcaagaagc gccagcggcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtc cgcacctca accaatcggg gaaccaccag caggccctc tggctctgga 600
tctgtgtaaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gcccttcaac 960

```

```

atccagggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
cttacctga acaatggaag tcaagccgta ggccgttcct cttctactg cctggaatat 1200
tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260
gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
atcgaccagt acctgcacta cttatccaga actcagtcca caggaggaac tcaagggtacc 1380
cagcaattgt tattttctca agctgggcct gcaaactatgt cggctcaggc taagaactgg 1440
ctacctggac cttgtaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500
agcaactttg cttggactgg tgccaccaa tatcacctga acggaagaga ctctttggta 1560
aatcccggcg tcgccatggc aaccacaaag gacgacgagg aacgcttctt cccgtcgagt 1620
ggagtcctga tgtttggaag acaggggtgct ggaagagaca atgtggacta cagcagcggt 1680
atgctaacca gcgaagaaga aattaaaacc actaacctg tagccacaga acaatacggg 1740
gtgtgtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca ggggtccatc 1860
tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgcta at gggaggattt 1920
ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980
ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
gtcagcgctg aaatcgagt ggagctgcag aaggagaaca gcaaacgctg gaaccagag 2100
attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
ggaacttatt ctgagcctcg cccattggg actcgctacc tcaccgtaa tctgtaa 2217

```

```

<210> 8
<211> 2217
<212> DNA
<213> new AAV serotype, clone hu.42

```

```

<400> 8
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc cgtcaacgc ggccgacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgcca cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag 360
gccaagaagc ggggtctcga acctctcggg ctggttgagg aagcggctaa gacggctcct 420
ggaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaag gccagcagcc cgctaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggcttggga 600
tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
atccagggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
cttacctga acaatggaag tcaagccgta ggccgttcct cttctactg cctggaatat 1200
tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

```

```

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaagggtacc 1380
cagcaattgt tatttttctca agctgggcct gcaaacaatgt cggctcaggc taagaactgg 1440
ctacctggac cttgttaccg gcagcagcga gtctctacga cactgtcgca aagcaacaac 1500
agcaactttg cttggactgg tgccaccaa taccacctga acggaagaga ctctttggta 1560
aatccccgtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcgagt 1620
ggagtcctga tgtttggaaa acaggttgct ggaagagaca atgtggacta cagcagcgtt 1680
atgctaacca gcgaagaaga aattaaaacc actaacctg tagccacaga acaatacggg 1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggccccatc 1860
tgggccaaga ttccctcacac ggacggcaac ttccaccctt caccgctaata gggaggactt 1920
ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccgggtacc tgcggatcct 1980
ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gaaacgctg gaaccagag 2100
attcagtaca cttcaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
ggaacttatt ctgagcctcg cccatttggg actcgttacc tcaccgtaa tctgtaa 2217

```

<210> 9
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.72

```

<400> 9
atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtgggggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctgggtct tcctgggtac aagtacctg gaccttcaa cggactcgac 180
aaggggggag cctgcaacgc ggcggacgca gcggccctg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaagc gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtc ccgacctca accaatcgga gaaccaccag caggccccctc tggcttggga 600
tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgcccag 660
ggagtggtga gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gacccgaac ctgggcctg cccacctaca acaaccact ctacaagcaa 780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt caacagattc cactgccact tctcaccag tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
atccaggcca aggaggtcac gcagaatgaa ggcaccaaga ccacgcgcaa taaccttacc 1020
agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgag 1080
caccagggtc gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
cttacctga acaatggaag tcaagccgta ggcggttctt cttctactg cctggaatat 1200
tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260
gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaagggtacc 1380
cagcaattgt tatttttctca agctgggcct gcaaacaatgt cggctcaggc taagaactgg 1440
ctacctggac cttgttaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500
agcaactttg cttggactgg tgccaccaa taccacctga acggaagaga ctctttggta 1560

```

```

aatccccggtg tcgccatggc aaccacacaag gacgacgagg aacgcttctt cccgtcgagt 1620
ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcggt 1680
atgctaacca gcgaagaaga aattaaaacc actaaccttg tagccacaga acaatacggg 1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca ggggtccatc 1860
tgggccaaga ttcttcacac ggacggcaac ttccaccctt caccgctaata gggaggattt 1920
ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccgggtacc tgcggatcct 1980
ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
gtcagcgctg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaaccacagag 2100
attcagtaca cttaaaacta ctacaaatct acaaattgtg actttgctgt caatacagag 2160
ggaacttatt ctgagcctcg ccccatgtgt actcgttacc tcaccgtaa tctgtaa 2217

```

```

<210> 10
<211> 2217
<212> DNA
<213> new AAV serotype, clone hu.37

```

```

<400> 10
atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtgggtgg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagac gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactctc caccggcatc 480
ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccccctc tggctctggga 600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaac ctgggcccctg cccacctaca acaaccacct ctacaagcaa 780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
atccagggtc aggggttcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
agcacgattc aggtatttac ggactcgga taccagctgc cgtacgtcct cggctccgag 1080
caccagggtc gcctgcctcc gttcccgagg gacgtcttca tgattcccca gtacggctac 1140
cttacctga acaatggaag tcaagccgta ggccgttcct ctttctactg cctggaatat 1200
tttccatctc aaatgctgag aactggaaac aattttgaat tcagctacac cttcgaggac 1260
gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaagggtacc 1380
cagcaattgt tattttctca agctgggcct gcaaaccatgt cggtctaggc taagaactgg 1440
ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500
agcaactttg cttggactgg tgccaccaa tatcacctga acggaagaga ctctttggta 1560
aatccccggtg tcgccatggc aaccacacaag gacgacgagg aacgcttctt cccgtcgagt 1620
ggagtcctga tgttcggaaa acagggtgct ggaagagaca atgtggacta cagcagcggt 1680
atgctaacca gcgaagaaga aattaaaacc actaaccttg tagccacaga acaatacggg 1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca ggggtccatc 1860

```

tgggccaaga	ttcctcacac	ggacggcaac	ttccaccctt	caccgcta	at	gggaggattt	1920
ggactgaagc	acccacctcc	tcagatcctg	atcaagaaca	cgccggtacc	tg	cggtatcct	1980
ccaacaacgt	tcagccaggc	gaaattggct	tccttcatta	cgagctacag	cacc	gggacag	2040
gtcagcgtgg	aaatcgagtg	ggagctgcag	aaggagaaca	gcaaacgctg	ga	accagag	2100
attcagtaca	cttcaaaacta	ctacaaatct	acaaatgtgg	actttgctgt	ca	atacagag	2160
ggaacttatt	ctgagcctcg	ccccattggg	actcgttacc	tcaccgtaa	tct	gtaa	2217

<210> 11
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone hu.40

<400> 11							
atggctgctg	acggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc		60
gagtgggtggg	acctgaaacc	tggagcccc	aagcccaagg	ccaaccagca	gaagcaggac		120
gacggccggg	gtctgggtgt	tcctggctac	aagtacctcg	gaccttcaa	cggactcgac		180
aagggggagc	ccgtcaacgc	ggcgagcgca	gcggccctcg	agcacgacaa	ggcctacgac		240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	accacgccga	cgccgagttt		300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag		360
gccaagaagc	gggttctcga	acctctcggt	ctgggtgagg	aagctgctaa	gacggctcct		420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcatc		480
ggcaagaaag	gccagcagcc	cgctaaaaag	agactgagct	ttggtcagac	tggcgactca		540
gagtcagtcc	ccgacctca	accaatcgga	gaaccaccag	caggccccctc	tggctctggga		600
tctgtacaa	tggctgcagg	cggtggcgct	ccaatggcag	acaataacga	aggcgccgac		660
ggagtgggta	gttctctcag	aaattggcat	tgcgattcca	catggctggg	cgacagagtc		720
atcaccacca	gcaccgaac	ctgggcccctg	cccacctaca	acaaccacct	ctacaagcaa		780
atatccaatg	ggacatcggg	aggaagcacc	aacgacaaca	cctacttcgg	ctacagcacc		840
ccctgggggt	atthtgaact	caacagattc	cactgccact	tctcaccacg	tgactggcag		900
cgactcatca	acaacaactg	gggattccgg	ccaaaagac	tcagcttcaa	gctcttcaac		960
atccagggtca	aggaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taaccttacc		1020
agcacgattc	aggatattac	ggactcggaa	taccagctgc	cgtagctcct	cggctccgcy		1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattccccca	gtacggctac		1140
cttactactga	acaatggaag	tcaagccgta	ggccgttccct	ccttctactg	cctggaatat		1200
tttccatctc	aaatgctgcy	aactggaaac	aattctgaat	tcagctacac	cttcgaggac		1260
gtgcctttcc	acagcagcta	cgcacacagc	cagagcttgg	accgactgat	gaatcctctc		1320
atcgaccagt	acctgtacta	cttatccaga	actcagtcca	caggagggaac	tcaagggtacc		1380
cagcaattgt	tattttctca	agctgggcct	gcaaacatgt	cggctcaggc	taagaactgg		1440
ctacctggac	cttgctaccg	gcagcagcga	gtctctacga	cactgtcgca	aaacaacaac		1500
agcaactttg	cttggtgactg	tgccaccaa	tatcacctga	acggaagaga	ctctttggta		1560
aatcccgggtg	tcgccatggc	aaccacacaag	gacgacgagg	aacgcttctt	cccgtcgagt		1620
ggagtccctga	tgtttggaag	acaggggtgct	ggaagagaca	atgtggacta	cagcagcgtt		1680
atgctaacca	gcgaagaaga	aattaaaacc	actaacctg	tagccacaga	acaatacggg		1740
gtggtggctg	acaacttgca	gcaaaccaat	acagggccta	ttgtgggaaa	tgtcaacagc		1800
caaggagcct	tacctggcat	ggcttggcag	aaccgagacg	tgtacctgca	gggtcccac		1860
tgggccaaga	ttcctcacac	ggacggcaac	ttccaccctt	caccgcta	at	gggaggattt	1920
ggactgaagc	acccacctcc	tcagatcctg	atcaagaaca	cgccggtacc	tg	cggtatcct	1980
ccaacaacgt	tcagccaggc	gaaattggct	tccttcatta	cgagctacag	cacc	gggacag	2040
gtcagcgtgg	aaatcgagtg	ggagctgcag	aaggagaaca	gcaaacgctg	ga	accagag	2100
attcagtaca	cttcaaaacta	ctacaaatct	acaaatgtgg	actttgctgt	ca	atacagag	2160

ggaacttatt ctgagcctcg cccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 12
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone hu.38

<400> 12
 atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
 gagtggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcttacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag 360
 gccagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
 gagtcagtcc ccgacctca accaatcgga gaaccacctg caggccccctc tggctcggga 600
 tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
 ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaccgaac ctgggcccctg cccacctaca acaaccacct ctacaagcaa 780
 atatccaatg ggacatcggg agggagcacc aacgacaaca cctacttcgg ctacagcacc 840
 ccctgggggt attttgactt caacagattc cactgccact tctcaccag tgactggcag 900
 cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
 atccagggtca aggaggctac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
 agcagattc aggtatttac ggaactcgaa taccagctgc cgtacgtcct cggctccgag 1080
 caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattccca gtacggctac 1140
 cttacactga acaatggaag tcaagccgta ggccgttcct cttctactg cctggaatat 1200
 tttccatctc aaatgctcgc aactggaaac aattttgaat tcagctacac cttcgaggac 1260
 gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
 atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaaac tcaagggtacc 1380
 cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440
 ctacctggac cttgtaccg gcagcagcga gtctctacga cactgtcga aaacaacaac 1500
 agcaactttg cttggactgg tgccaccaa tatcacctga acggaagaga ctctttggta 1560
 aatcccgggtg tcgccatggc aaccacaaag gacgacgagg aacgcttctt cccgtcagat 1620
 ggagtctga tgtttgaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680
 atgctaacca gcgaagaaga aattaaaacc actaacctg tagccacaga acaatacggg 1740
 gtggtggctg acaacttgca gcaaaccat acagggccta ttgtgggaaa tgtcaacagc 1800
 caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggccccatc 1860
 tgggccaaga ttcctcacac ggacggcaac tgccaccctt caccgctaata gggaggattt 1920
 ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccgggtacc tgcggatcct 1980
 ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
 gtcagcgtgg aaatcagtg ggagctgcag aaggagaaca gcaaagcgtg gaaccagag 2100
 attcagtaca cttcaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
 ggaacttatt ctgagcctcg cccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 13
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.39
 <400> 13

atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaac gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
 gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggctcggga 600
 tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
 ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
 atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
 ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
 cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
 atccagggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
 agcacgattc aggtatttac ggactcgga taccagctgc cgtacgtcct cggctccgcg 1080
 caccagggct gcctgcctcc gttccggcg gacgtcttca tgattccca gtacggctac 1140
 cttacactga acaatggaag tcaagccgta ggccgttctt ctttctactg cctggaatat 1200
 tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260
 gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
 atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaagggtacc 1380
 cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440
 ctacctggac cttgtctacc gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500
 agcaactttg cttggactgg tgccaccaa tatcacctga acggaagaga ctctttggta 1560
 aatcccgggt tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcgagt 1620
 ggagtcctga tgtttggaac acaggggtgct ggaagagaca atgtggacta cagcagcgtt 1680
 atgctaacca gcgaagaaga aattaaaacc actaacctg tagccacaga acaatacggg 1740
 gtggtggctg ataacttgca gcaaaccaat acggggccta ttgtgggaaa tgtcaacagc 1800
 caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca ggggtccatc 1860
 tgggccaaga ttctctacac ggacggcaac ttccacctt caccgcta at gggaggattt 1920
 ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccgggtacc tgcggatcct 1980
 ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
 gtcagcgtgg aaatcgagt ggagctgcag aaggagaaca gcaaacgctg gaaccagag 2100
 attcagtaca cttcaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
 ggaacttatt ctgagcctcg cccattggg actcgttacc tcaccgtaa tctgtaa 2217

<210> 14
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.40

<400> 14
 atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc ggggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
 gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggcttggga 600
 tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
 ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
 atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
 ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
 cgactcatca acaacaactg gggattccg ccaaaaagac tcagcttcaa gctcttcaac 960
 atccagggtca aggaggtcac gcaggatgaa ggcaccaaga ccacgcgcaa taaccttacc 1020
 agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgag 1080
 caccagggtc gcctgcctcc gttcccgagg gacgtcttca tgattcccca gtacggctac 1140
 cttacactga acaatggaag tcaagccgta ggccgttctt cttctactg cctggaatat 1200
 tttccatctc aaatgctcgc aactggaaac aattttgaat tcagctacac cttcgaggac 1260
 gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
 atcgaccagt acctgtacta cttatccaga actcagtcga caggaggaac tcaagggtacc 1380
 cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcgggc taagaactgg 1440
 ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500
 agcaactttg cttggactgg tgccaccaa tatcacctga acggaagaga ctctttggta 1560
 aatcccggtg ttgctatggc aacgcataag gacgacgagg aacgtttctt tccatcgagc 1620
 ggagtctga tgtttgaaa acagggtgct ggaagagaca atgtggacta tagcagcgtt 1680
 atgctaacca gcgaggaaga aattaaaacc actaacctg tagccacaga acaatacggg 1740
 gtggtggctg acaacttgca gcaagccaat acagggccta ttgtgggaaa tgtcaacagc 1800
 caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca ggggtccatc 1860
 tgggcaaaa ttcctcacac ggacggcaat ttaccacctg ctctctgat gggcggcttt 1920
 ggactgaagc acccacctcc ccagatcctg atcaagaata cgccggtacc tgcggatcct 1980
 ccaacgacgt tcagccaggc aaaattggct tccttcatca cgcagtacag caccggccag 2040
 gtcagcgtg agatcgagt ggagctgcag aaggagaaca gcaagcgatg gaaccagaa 2100
 attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caattctgag 2160
 ggtacatatt cagagcctcg cccattggg actcgttattc tgacacgtaa tctgtaa 2217

<210> 15

<211> 2217

<212> DNA

<213> new AAV serotype, clone rh.64

<400> 15

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtgggtgg acctgaaacc tggagccccg aaacccaag ccaaccagca aaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctc gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctc agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc ggggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
 gagtcagtcc ccgacctca acctatcgga gaacctccag cagcgcctc tagtggtggga 600

tctggtacaa	tggctgcagg	cggtggcgca	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctacttttg	ctacagcacc	840
ccctgggggt	attttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattcccg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccaggtca	aagaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcacc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagctgc	cgtacgtcct	cggctctgcc	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttcccccttc	agatgctgag	aacgggcaac	aacttttctt	tcagctacac	tttcgaggac	1260
gtgccttttc	acagcagcta	cgcgcacagc	cagagtgttg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	acccagtcta	cgaggaggac	agcgggaacc	1380
cagcagttgc	tgttttctca	ggccgggcct	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctgggtg	1560
aatccgggcg	tcgccatggc	aaccaacaag	gacgacgagg	accgcttctt	cccatccagc	1620
ggcatcctca	tgtttggcaa	gcaggggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaaac	accgctccta	ttgtgggggc	cgtcaacagc	1800
cagggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttctcacac	agatggcaac	tttcaccgt	ctcctttaat	gggcggcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaca	ctcctgttcc	tgcggtatcct	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatca	cgcagtacag	caccggacaa	2040
gtcagcgtgg	agatcgtgtg	ggagctgcag	aaggagaaca	gcaagcgcag	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgctgt	taatactgag	2160
ggtgtttact	ctgagcctcg	ccccattggc	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 16
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.68

<400> 16						
atggctgccc	atggttatct	tccagattgg	ctcaggagaca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	atcacgccga	cgccaggttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcac	480
ggcaagaaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcagac	tggcgactca	540
gagtcagtcc	ccgaccttca	acctatcgga	gaacctccag	cagcgccttc	tagtgtggga	600
tctggtacaa	tggctgcagg	cggtggcgca	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctgggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctacttttg	ctacagcacc	840
ccctgggggt	attttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900

```

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
caccagggct gcctgcctcc gtccccggcg gacgtcttca tgattcctca gtacggctac 1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct cttctactg cctggagtac 1200
ttcccccttc agatgctgag aacgggcaac aacttttcct tcagctacac tttcaggagac 1260
gtgcctttcc acagcagcta cgcgcacagc cagagtgttg acaggctgat gaatcctctc 1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380
cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440
ctgcctggac cctgtctacg acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccaccacgc 1620
ggcatcctca tgttttgcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtggggc cgtcaacagc 1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt 1860
tgggccaaga ttcttcacac agatggcaac tttcaccgt ctctttaa gggcggttt 1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct 1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040
gtcagcgtgg tgatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160
ggtgtttact ctgagcttcg ccccatggc actcgttacc tcaccgtaa tctgtaa 2217

```

```

<210> 17
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.53

```

```

<400> 17
atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcttacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagaag gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccgtcaccà cagcgttccc ccgactcctc cacgggcattc 480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcgggtcagac tggcgactca 540
gagtcagtcc ccgacctca acctatcgga gaacctccag cagcgccctc tagtggtgga 600
tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac 660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
caccagggct gcctgcctcc gtccccggcg gacgtcttca tgattcctca gtacggctac 1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct cttctactg cctggagtac 1200

```

```

ttccccctctc agatgctgag aacgggcaac aacttttctc tcagctacac tttcgaggac 1260
gtgcctttcc acagcagcta cgtgcacagc cagagtttgg acaggctgat gaatcctctc 1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380
cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560
aattcgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
ggcatcctca tgtttggcaa gcaggagct ggaagagaca acgtggacta tagcaacgtg 1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc 1800
caggggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt 1860
tgggccaaga ttcctcacac agatggcaac tttcaccctg ctctcttaat gggcggcttt 1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct 1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160
ggtgtttact ctgagcctcg cccattggc actcgttacc ccaccgtaa tctgtaa 2217

```

```

<210> 18
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.52

```

```

<400> 18
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctggtgct tcttggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600
tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac 660
ggagtgggta gttctctcgg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaac ctgggcctcg ccacctaca acaaccacct ctacaagcaa 780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840
ccctgggggt attttgactt taacagattc cactgccact tctcaccag tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaagagac tcagcttcaa gctcttcaac 960
atccagggtca aagaggctac gcagaatgaa ggcaccaaga ccatcgccaa tagcctcacc 1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140
ctgactccca acaacggtag tcaggccgtg ggagcttctt cttctactg cctggagtac 1200
ttccccctctc agatgctgag aacgggcaac aacttttctc tcagctacac tttcgaggac 1260
gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380
cagcagttgc tgtcttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

```

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560
 aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
 ggcacatctca tgtttgga gacgggagct ggaaaagaca acgtggacta tagcaacgtg 1680
 atgctaacca gcgaggaaga aatcaagacc accaaccctg tgccacaga acagtatggc 1740
 gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc 1800
 caggggagcct tacctggcat ggtctggcag aaccgggacg tgtacttgca gggtcctatt 1860
 tgggccaaga ttcctcacac agatggcaac ttccaccctg ctctcttaac gggcggcttt 1920
 ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct 1980
 ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040
 gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100
 attcagtata cttccaacta ctacaaatct acaaatgtgg actttgtgt taatactgag 2160
 ggtgtttact ctgagcctcg cccattggc actcgttacc tcaccgtaa tctgtaa 2217

<210> 19
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.46

<400> 19
 atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtgggtgg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
 gacggccggg gtctgggtct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgcgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccagaagc gggttctcga acctctcggc ctggttgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc caccggcatc 480
 ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
 gagtcatgcc ccgacctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600
 tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac 660
 ggagtgggta gtctctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gacccgaac ctgggcccctg ccacacctca acaaccacct ctacaagcaa 780
 atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840
 ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgaactggcag 900
 cgactcatca acaacaactg gggattccgg ccaagagac tcagcttcaa gctcttcaac 960
 atccagggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020
 agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
 caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140
 ctgacttca acaacggtag tcaggccgtg ggacgttcct cttctactg cctggagtac 1200
 ttccctctc agatgctgag aacgggcaac aacttttcct tcagctacac ttctgaggac 1260
 gtgcctttcc acagcagcta cgcgcacagc cagagtgttg acaggctgat gaatcctctc 1320
 atcgaccagt acctgtacta cctgtcaaga acccagctca cgggaggcac agcgggaacc 1380
 cagcagttgc tgtttttca ggcgggacct agcaacatgt cggctcaggc cagaaactgg 1440
 ctgcctggac cctgtacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
 agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560
 aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
 ggcacatctca tgtttgga gacgggagct ggaaaagaca acgtggacta tagcaacgtg 1680
 atgctaacca gcgaggaaga aatcaaggcc accaaccctg tgccacaga acagtatggc 1740
 gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt	1860
tgggccaaga ttcttcacac agatggcaac ttccacccgt ctcctttaat gggcggcttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag	2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag	2160
ggtgtttact ctgagcctcg ccccatgtgc actcgttacc tcaccgtaa tctgtaa	2217

<210> 20
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.70

<400> 20	
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct	420
ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc	480
ggcaagaagc gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca	540
gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga	600
tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac	660
ggagtgggta gtctctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcaccgaac ctgggccctg cccgcctaca acaaccacct ctacaagcaa	780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960
atccaggtea aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc	1020
agcaccatcc aggtgtttac ggactcgga taccagctgc cgtacgtcct cggctctgcc	1080
caccagggct gcctgcctcc gttcccggcg gatgtcttca tgattcctca gtacggctac	1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac	1200
ttcccctctc agatgctgag aacgggcaac aacttttctt tcagctacac ttctcaggac	1260
gtgccttttc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc	1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc	1380
cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg	1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac	1500
agcaactttg cctggactgg tgccaccaag tatcatctga gcggcagaga ctctctgggtg	1560
aatccgggcy tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc	1620
ggcatcctca tgtttggcaa gcaggggact ggaaaagaca acgtggacta tagcaacgtg	1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc	1740
gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc	1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt	1860
tgggccaaga ttcttcacac agatggcaac ttccacccgt ctcctttaat gggcggcttt	1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct	1980
ccaacagcgt tcaaccaggc caagctgaat tcttccatca cgcagtacag caccggacaa	2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag	2100

```

attcāgtātā cttccaacta ctacaaatct acaaagtgg actttgctgt taatactgag 2160
ggtgtttact ctgagcctcg ccccatgtggc actcgttacc tcaccgtaa tttgtaa 2217

<210> 21
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.61

<400> 21
atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtggtggg acctgaaacc tggagccccg aaaccaagg ccaaccagca aaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcgccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagaag gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
gagtcagtcc ccgacctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600
tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
cgacctatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
atccagggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
caccagggct gcctgcctcc gttcccgcg gacgtcttca tgattcctca gtacggctac 1140
ctgacttca acaacggtag tcaggccgtg ggacgttctt ctttctactg cctggagtac 1200
ttccctctc agatgctgag aacgggcaac aacttttctt tcagctaccc tttcgaggac 1260
gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggtgat gaatcctctc 1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380
cagcagttgc tgttttctca ggcgggcct agcaacatgt cggctcaggc cagaaactgg 1440
ctgcctggac cctgtacag acagcagcgt gtctccacga cactgtcgca aaacaacaac 1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
gtggtggctg ataacctaca gcagcaagac accgctccta ttgtgggggc cgtcaacagc 1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt 1860
tgggccaaga ttcctcacac agatggcaac tttcaccctg ctcttttaat gggcggcttt 1920
ggacttaaac atccgcctcc tcaggctctc atcaaaaaca ctctgttcc tgcggatcct 1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100
attcagtata cttccaacta ctacaaatct acaaagtgg actttgctgt taatactgag 2160
ggtgtttact ctgagcctcg ccccatgtggc actcgttacc tcaccgtaa tctgtaa 2217

```

```

<210> 22
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.51

```

<400> 22

atggttgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtgggagg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcagggc 120
 gacggccggg gtctgggtgt tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctta aagcgggtga caatccgtac ctgcggtata atcacgccga cgcgagctt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaac ggggttctga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc cgcactctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgcagaaaag agactcaatt tcggtcagac tggcgactca 540
 gagtcatgcc ccgacctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600
 tctgggtacaa tggctgcagg cgggtggcgc ccaatggcag acaataacga aggtgccgac 660
 ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
 atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840
 ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
 cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
 atccagggtca aagaggtcac gcagaatgaa ggcaccaaga ccacgcgcaa taacctcacc 1020
 agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
 caccagggct gccagcctcc gttccggcg gacgtcttca tgattcttca gtacggctac 1140
 ctgactctca acaacggtag tcaggccgtg ggacgttctt ccttctactg cctggagtac 1200
 ttccctctc agatgctgag aacgggcaac aacttttctt tcagctacac tttcgaggac 1260
 gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320
 atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380
 cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440
 ctgcctggac cctgtacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
 agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctgggtg 1560
 aatccggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
 ggcatcctca tgtttggcaa gcaggggagct ggaaaagaca acgtggacta tagcaacgtg 1680
 atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
 gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc 1800
 caggggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt 1860
 tgggccaaga ttcttcacac agatggcaac tttcaccgt ctctttaaag gggcggcttt 1920
 ggacttaaac atccgcctcc tcagatctc atcaaaaaca ctctgttcc tgcggatcct 1980
 ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040
 gtcagcgtgg agatcgagtg ggagccgcag aaggagaaca gcaagcgtg gaaccagag 2100
 attcagtata ctccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160
 ggtgtttact ctgagcctcg cccatttggc actcgttacc tcaccgtaa tctgtaa 2217

<210> 23

<211> 2217

<212> DNA

<213> new AAV serotype, clone rh.50

<400> 23

atggttgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtgggagg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
 gacggccggg gtctgggtgt tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgcgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc ggggttctcga acctctcggg ctgggtgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgccggaaag agactcaatt tcggtcagac tggcgactca 540
 gagttagtcc ccgacctca acctatcgga gaacctccag cagcgcctc tagtgtggga 600
 tctggtacaa tggctgcagg cgggtgcgca ccaatggcag acaataacga aggtgccgac 660
 ggagtgggta gttctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaccgaac ctgggacctg cccacctaca acaaccacct ctacaagcaa 780
 atctccaacg ggacctcggg aggcagcacc aacgacaaca cctacttttg ctacagcacc 840
 ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
 cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
 atccagggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020
 agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
 caccaggggt gcctgcctcc gttcccgcg gacgtcttca tgattcctca gtacggctac 1140
 ctgacttca acaacggtag tcaggccgtg ggacgttctt ccttctactg cctggagtac 1200
 tttccctctc agatgctgag aacgggcaac aacttttctt tcagctacac tttcgaggac 1260
 gtgcctttcc acagcagcta cgcgcacagc cagagtgttg acaggctgat gaatcctctc 1320
 gtcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380
 cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440
 ctgcctggac cctgtctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
 agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctgggtg 1560
 aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
 ggcacctca tgtttggcaa gcaggagct ggaaaagaca acgtggacta tagcaacgtg 1680
 atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
 gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc 1800
 caggggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggctctatt 1860
 tggggcaaga ttcctcacac agatggcaac tttcaccctg ctcttctaag gggcggtttt 1920
 ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct 1980
 ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040
 gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gagccagag 2100
 attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160
 ggtgtttact ctgagcctcg cccattggc actcgttacc tcaccgtaa tctgtaa 2217

<210> 24
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone hu.39

<400> 24
 atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtggggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
 gacggccggg gtctgggtgt tcttggttac aagtacctg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc ggggttctcga acctctcggg ctgggtgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcggac tggcgactca 540
 gagttagtcc ccgacctca acctatcgga gaacctccag cagcgcctc tagtgtggga 600

tctggtacaa	tggctgcagg	cggtggcgca	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtt	720
atcaccacca	gcaccgaac	ctggggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctactttgg	ctacagcacc	840
ccctgggggt	atcttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aagagggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcgcc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagccgc	cgtacgtcct	cggtcttgcc	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtac	1200
ttcccccttc	agatgctgag	aacgggcaac	aacttttctt	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	acccagtcta	cgggaggcac	agcgggaacc	1380
cagcagttgc	tgttttctcg	ggccgggcct	agcaacatgt	cggtcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	cactgtcgca	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccgggcg	tcgccatggc	aaccaacaag	gacgacgagg	accgcttctt	cccatccagc	1620
ggcatcctca	tgtttggtgca	gcagggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccg	tgccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaac	accgctccta	ctgtgggggc	cgtcaacagc	1800
cagggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttcctcacac	agatggcaac	tttcaccctg	ctcctttaat	gggcggcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaca	ctcctgttcc	tgcggtatcct	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatcg	cgcagtacag	caccggacaa	2040
gtcagcgtgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgtg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgcgg	actttgctgt	taatactgag	2160
gggtgtttact	ctgagcctcg	ccccattggc	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 25
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.49

<400> 25						
atggctgccg	atggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagcccg	aaacccaaag	ccaaccagca	aaagcaggac	120
gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgcac	ctgcggtata	atcacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaaagaag	gggttctcga	acctctcggg	ctgggtgagg	aaggcgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcatc	480
ggcaagaag	gccagcagcc	cgccagaaag	agactcaatt	tcggtcagac	tggcgactca	540
gagtcagtcc	ccgacctcta	acttatcgga	gaacctccag	cagcgccctc	tagtgtggga	600
tctggtacaa	tggctgcagg	cggtggcgca	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcaccgaac	ctggggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctactttgg	ctacagcacc	840
ccctgggggt	atcttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
 atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020
 agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgtcct cggctctgcc 1080
 caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggcaac 1140
 ctgactctca acaacggtag tcaggccgtg ggacgttcct ctttctactg cctggagtac 1200
 ttcccccttc agatgtctgag aacgggcaac aacttttcct tcagctacac tttcaggagac 1260
 gtgcctttcc acagcagcta cgcgcacagc cagagtgttg acaggctgat gaatcctctc 1320
 atcgaccagt acctgtacta cctgtcaaga acccagctta cgggaggcac agcgggaacc 1380
 cagcagttgc tgtttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440
 ctgcctggac cctgtctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
 agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctgggtg 1560
 aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
 ggcacctctca tgtttggcaa gcaggaggt ggaaaagaca acatgggcta tagcaacgtg 1680
 atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
 gtggtggctg ataacctaca gcagcaaac accgtccta ttgtgggggc cgtcaacagc 1800
 caggagcct tacctggcat ggtctggcag aaccgggacg tgtacctga gggctctatt 1860
 tgggccaaga ttcctcacac agatggcaac tttcaccctg ctctttaa gggcggttt 1920
 ggacttaaac atccgcctcc tcagatcttc atcaaaaaca ctctgttcc tgcggatcct 1980
 ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacgg caccggacaa 2040
 gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100
 attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160
 ggtgtttact ctgagcctcg cccattggc actcgttacc tcaccgtaa tctgtaa 2217

<210> 26
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.57

<400> 26
 atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtgggtgg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctgc aggcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaag gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcattc 480
 ggcaagaaag gccagcagcc gccagaaag agactcaatt tcggtcagac tggcgactca 540
 gagtcatgcc ccgacctca acctatcggg gaacctccag cagcgccctc tagtgtggga 600
 tctgttacia tggctgcagg cgggtggcgc ccaatggcag acaataacga aggtgccgac 660
 ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaccgaac ctgggcccctg cccacctaca acaaccacct ctacaagcaa 780
 acctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840
 ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900
 cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
 atccagggtca aagagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020
 agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
 caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140
 ctgactctca acaacggtag tcaggccgtg ggacgttcct ctttctactg cctggagtac 1200

ttccccctctc	agatgctgag	aacgggcaac	aacttttctc	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	accagctcta	cgggaggcac	agcgggaacc	1380
cagcagttgc	tgttttctca	ggccgggctt	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	caactgtcga	aaacaacaac	1500
agcaactttg	cctggactgg	tgccaccaag	tatcatctga	acggcagaga	ctctctggtg	1560
aatccgggcg	tcgcatggc	aaccaacaag	gacgacgagg	accgcttctt	cccatccagc	1620
ggcatcctca	tgtttggcaa	gcagggagct	ggaaaagaca	acgtggacta	tagcaacgtg	1680
atgctaacca	gcgaggaaga	aatcaagacc	accaaccccc	tggccacaga	acagtatggc	1740
gtggtggctg	ataacctaca	gcagcaaaac	accgctccta	ttgtgggggc	cgtaacagc	1800
cagggagcct	tacctggcat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcctatt	1860
tgggccaaga	ttcctcacac	agatggcaac	ttcaccctgt	ctcctttaat	ggcggtcttt	1920
ggacttaaac	atccgcctcc	tcagatcctc	atcaaaaaca	ctcctgttcc	tcgggatcct	1980
ccaacagcgt	tcaaccaggc	caagctgaat	tctttcatca	cgcagtacag	caccggacaa	2040
gtcagcgcgg	agatcgagtg	ggagctgcag	aaggagaaca	gcaagcgtg	gaaccagag	2100
attcagtata	cttccaacta	ctacaaatct	acaaatgtgg	actttgctgt	taatactgag	2160
ggtgtttact	ctgagcctcg	ccccattggc	actcgttacc	tcaccgtaa	tctgtaa	2217

<210> 27

<211> 2217

<212> DNA

<213> new AAV serotype, clone rh.58

<400> 27

atggctgctg	acggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
gagtgggtgg	acctgaaacc	tggagcccc	aagcccaagg	ccaaccagca	gaagcaggac	120
gacggccggg	gtctggtgct	tcttggctac	aagtacctcg	gacccttcaa	cggactcgac	180
aagggggagc	ccgtcaacgc	ggcggagcga	gcggccctcg	agcacgacaa	ggcctacgac	240
cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	atcacgccga	cgccgagttt	300
caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	360
gccaaagaag	gggttctcga	acctctcggg	ctggttgagg	aagctgctaa	gacggctcct	420
ggaaagaaga	gaccggtaga	accgtcacct	cagcgttccc	ccgactcctc	cacgggcatc	480
ggcaagaaag	gccagcagcc	cgctagaaag	agactgaact	ttgggcagac	tggcgactca	540
gagtcagtcc	ccgacctca	accaatcgga	gaacctccag	cagcgccctc	tagtgtggga	600
tctggtacaa	tggcgcgagg	cgggtggcga	ccaatggcag	acaataacga	aggtgccgac	660
ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
atcaccacca	gcacccgaac	ctgggcccctg	cccacctaca	acaaccacct	ctacaagcaa	780
atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctactttgg	ctacagcacc	840
ccctgggggt	attttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
cgactcatca	acaacaactg	gggattccgg	ccaagagac	tcagcttcaa	gctcttcaac	960
atccagggtca	aagaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taacctcacc	1020
agcaccatcc	aggtgtttac	ggactcggaa	taccagctgc	cgtacgtcct	cggctctgcc	1080
caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcctca	gtacggctac	1140
ctgactctca	acaacggtag	tcaggccgtg	ggacgttcct	ccttctactg	cctggagtag	1200
ttccccctctc	agatgctgag	aacgggcaac	aacttttctc	tcagctacac	tttcgaggac	1260
gtgcctttcc	acagcagcta	cgcgcacagc	cagagtttgg	acaggctgat	gaatcctctc	1320
atcgaccagt	acctgtacta	cctgtcaaga	accagctcta	cgggaggcac	agcgggaacc	1380
cagcagctgc	tgttttctca	ggccgggctt	agcaacatgt	cggctcaggc	cagaaactgg	1440
ctgcctggac	cctgctacag	acagcagcgc	gtctccacga	caactgtcga	aaacaacaac	1500

```

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
ggcatcctca tgtttggcaa gcaggagagct ggaaaagaca acgtggacta tagcaacgtg 1680
atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800
caggggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860
tgggccaaga ttcttcacac agatggcaac tttcacccgt ctcttttaat gggcggcttt 1920
ggacttaaac atccgcctcc tcagatcctc atcaaaagca ctctgttcc tgcggatcct 1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040
gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagtgtg gaaccagag 2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160
ggtgtttact ctgagcctcg cccatttggc actcgttacc tcaccgtaa tctgtaa 2217

```

```

<210> 28
<211> 2196
<212> DNA
<213> new AAV serotype, clone pi.1

```

```

<400> 28
atggctgtg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtgggtgg cgctgaaacc tggagcccg caacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgggtgt tcttggttac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgcgagttt 300
caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttcag 360
gccaaaaaga gggtaactga gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaagc ggcagtaga accggactcc agctcgggca tcggcaagtc aggccagcag 480
cccgcaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc 540
caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgct 600
ggcgggtggc ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca 660
ggaaattggc attgcgattc cacatggctg ggcgaccgag tcaccaccac cagcactcgg 720
acctggggcc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780
ggaggcagca gcaacgacaa cacctacttt ggctacagca cccctgggg gtattttgac 840
ttaacagat tccactgcca cttttacca cgtgactggc agcgactcat caacaacaac 900
tgggggttcc ggcccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960
accagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggctctt 1020
acggactcgg agtaccagct cccgtacgtg ctcggtctcg cccaccaggg ctgctgcct 1080
ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140
agccaggccg tggggcgatc ctcttcttac tgcttgaggt actttccctc gcagatgctg 1200
agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260
tacgcgcaca gccagagcct ggaccggctg atgaaccgc tgattgacca gtacctgtac 1320
tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380
gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcttggtcc ttgctatcgg 1440
cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500
gcgaccaagt accacctgaa cggccgagac tccctgggtg gcccgggtgt cgccatggca 1560
acgcacaagg acgacgagga gcgttcttcc ccgagcagcg gggtcctgat gtttgcaag 1620
cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680
atcaagacca ccaacctgtg ggccacggag cagtacggcg tgggtggctg caatctgcag 1740
cagaccaact cagctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

```

```

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860
gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920
cagatcctga tcaaaaacac gccggtacct gcggtatccc cggatgaactt tacggacgct 1980
aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040
gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100
tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccg 2160
cccattggca ctcgttacct caccgtaat ctgtaa 2196

```

```

<210> 29
<211> 2196
<212> DNA
<213> new AAV serotype, clone pi.3

```

```

<400> 29
atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtgggggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgggtct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aaggggggag ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaaaaga ggggtactcg gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag 480
cccgcgaaaa agagactgaa ttttgggccc actggcgact cagagtcagt gcctgacccc 540
caacctctct cagaaccacc tgcaggctcc tctggctctg gatctggtac aatggctgca 600
ggcggtgggc ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca 660
ggaaattggc attgcgattc cacatggctg ggcgaccgag tcataccac cagcactcgg 720
acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780
ggaggcagca gcaacgacaa cacctacttt ggctacagca cccctgggg gtattttgac 840
tttaacagat tccactgcca cttttacca cgcgactggc agcgactcat caacaacaac 900
tggggattcc ggccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960
accagaatg aaggcaccaa gaccaccgcc aataacctca ccagcacggt gcaggctctt 1020
acggactcgg agtaccagct cccgtacgtg ctcggtctg cccaccaggg ctgcctgcct 1080
ccgttcccgg cggacgtggt catgattccg cagtacgggt acctgacgct gaacaacggg 1140
agccaggccg tggggcgatc ctcttcttac tgcctggagt actttccctc gcagatgctg 1200
agaacgggca acaactttac cttcagctat accttcgagg acgtgccctt ccacagcagc 1260
tacgcgcaca gccagagcct ggaccggctg atgaaccgcg tgattgacca gtacctgtac 1320
tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380
gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440
cagcagcgcg tctctacggc agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500
gcgaccaagt accacctgaa cggccgagac tccctggtga accccgggtg cgccatggca 1560
acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggctctgat gtttggaag 1620
cagggcgctg gaaaggacaa tgtcgagta accaactgta tgctcaccag cgaggaggag 1680
atcaagacca ccaacctgt ggccacggag cagtacgggt tgggtggtga caatctgcag 1740
cagaccaact cggctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800
gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860
gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920
cagatcctga tcaaaaacac gccggtacct gcggtatccc cggatgaactt tacggacgct 1980
aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040
gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

```

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag cgaaccccg 2160
cccattggca ctcgttacct caccgtaat ctgtaa 2196

<210> 30
<211> 2196
<212> DNA
<213> new AAV serotype, clone pi.2

<400> 30
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtgg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgggtgt tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacga ggcgagcgcc gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgcgaggttt 300
caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaaaaga gggctactga gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccggcag 480
cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc 540
caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgca 600
ggcgggtggc ctccaatggc agacaataac gaaggcgccg acggagtggg taatgcctca 660
ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720
acctggggcc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780
ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840
tttaacagat tccactgcca cttttacca cgtgactggc agcgactcat caacaacaac 900
tggggattcc ggcccaagag gctcaacttc aagctcttca acatccaggt caaggaggtc 960
accagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggtcttt 1020
acggactcga agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080
ccgttcccgg cggacgtggt catgattccg cagtacgggt acctgacgct gaacaacggg 1140
agccaggccg tggggcgatc ctcttctac tgctggagt actttccctc gcagatgctg 1200
agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260
tacgcgcaca gccagagcct ggaccggctg atgaaccgcg tgattgacca gtacctgtac 1320
tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380
gccgggcttc agaacatgtc ggctcaggcc aagaactggc tgcttggtcc ttgctatcgg 1440
cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500
gcgaccaagt accacctgaa cggccgagac tccctggtga accccgggtg cgcctatggca 1560
acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggctctgat gtttggaag 1620
cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680
atcaagacca ccaaccctgt ggccacggag cagtacgggt tgggtgctga caatctgcag 1740
cagaccaact cggctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800
gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860
gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920
cagatcctga tcaaaaacac gccggtacct gcggatcccc cgggtgaactt tacggacgct 1980
aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040
gagctgcaga aggagaacag caagcgtggt aatcccgaga ttcagtacac ttccaattat 2100
tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccg 2160
cccattggca ctcgttacct caccgtaat ctgtaa 2196

<210> 31
<211> 2208
<212> DNA
<213> new AAV serotype, clone rh.60

<400> 31
 atggctgccc atgggttatct tccagattgg ctcgaggaca acctctctga gggcattcac 60
 gagtggtggg acccgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgcgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
 gagtcagtcc ccgacctca acctatcggg gaacctccag cagcgccctc tagtgtggga 600
 tctggtacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac 660
 ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaccgaaac ctgggccctg cccaccaca acaaccacct ctacaagcaa 780
 atctccaacg ggacctcggg aggcagcacc aacgacaacg tctacttcgg ctacagcacc 840
 ccctgggggt attttgactt caacagattc cactgtcact tctcaccacg tgaccggcag 900
 cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
 atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccacgcca taacctcacc 1020
 agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080
 caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140
 ctgactctca acaacggtag tcaggccgtg ggacgttccct ccttctactg cctggagtac 1200
 ttccccctc agatgctgag aacgggcaac aacttttccct tcagctacac tttcgaggac 1260
 gtgcctttcc acagcagcta cgcgcacagc cagagtttg acaggctgat gaatcctctc 1320
 atcgaccagt acctgtacta cctgtcaaga acccagtcta cggaaggcac agcgggaacc 1380
 cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440
 ctgcctggac cctgtctacg acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
 agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctgggtg 1560
 aatccgggcg tcgccatggc aaccacaaag gacgacgagg aacgcttctt cccttcgagc 1620
 ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
 atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact 1740
 gttagcagca acctgcaggc ggctaactact gcagcccaga cacaagttgt caacaaccag 1800
 ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860
 gccaaagattc ctacacagga cggcaacttt caccgtctc cgctgatggg cggctttgga 1920
 ctgaagcatc ctcatatcct gatcaaaaac actcctgttc ctgctaattc ccgagaggtg 1980
 tttacgcctg ccaagtgtgc ttctttcatc acacagtaca gcaccggcca ggtcagcgtg 2040
 gagatcgagt gggagctgca gaaggagaac agcaagcgtt ggaaccaga gattcagtat 2100
 acctcaatt ttgacaaaca gactggtgtg gactttgccg ttgacagcca ggggttttat 2160
 tctgagcctc gccccattgg tactcgttac ctacccgta atctgtaa 2208

<210> 32
 <211> 2214
 <212> DNA
 <213> new AAV serotype, clone rh.48

<400> 32
 atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtggtggg acctgaaacc tggagccccg aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

gagtagctca aagtcgggtga caattcgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540
 gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggctcggga 600
 tctggtacaa tggctgcagg cgggtggcga ccaatggctg acaataacaa gggcgccgac 660
 ggagtgggta atgctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaaccgaac ctgggctttg ccacacctaca acaaccacct ctacaagcaa 780
 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc 840
 tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
 ctcatcaaca gcaactgggg attccggccc aagaagctca attcaagct gttcaacatc 960
 cagggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020
 acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080
 cagggtgcc tgcctccgtt cccggcggac gtcttcatga tccccagta cggctacctg 1140
 actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200
 ctttctcaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260
 cccttcaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320
 gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
 cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440
 ctgcctggac ctgtcttcg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500
 agcaactttg cttggactgg tgccaccaa taccatctaa atggaagaaa ttcattgggt 1560
 aatcccgtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc 1620
 ggagtcctga tttttgaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
 atgacaaatg aagaggaaat tcgtcttacc aaccggtag ccaccgagga atacgggact 1740
 gttagcagca acctgcaggc ggctaact gcagcccaga cacaagttgt caacaaccag 1800
 ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860
 gccagattc ctcacacgga cggcaacttt caccgctctc cgctgatggg cggctttgga 1920
 ctgaagcatc cgctcctca gatcctgatc aaaaacactc ctgttctgc taatcccccg 1980
 gaggtgttta cgcttgcaa gtttgcctt ttcacacac agtacagcac cggccaggct 2040
 agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa ccagagatt 2100
 cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160
 gtttattctg agcctcgccc cattggtact cgttacctca ccgtaatct gtaa 2214

<210> 33
 <211> 2214
 <212> DNA
 <213> new AAV serotype, clone rh.62

<400> 33
 atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
 gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctgggtct tcctggctac aagtacctg gaccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctc agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttc 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtctagtc ccgaccctca accaatcggg gagccaccag caggccccctc tggctctggga 600
 tctggtacaa tggctgcagg cgggtggcgca ccaatggctg acaataacaa gggcgccgac 660
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780
 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840
 tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
 ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960
 cagggtcaagg aggtcacaac ggggtgacggc gtcacgacca tcgccaataa cttaccagc 1020
 acggttcagg tcttttcgga ctccgaatac cagctgccct acgtcctcgg ctccgcacac 1080
 cagggtctgcc tgcctccgtt cccggcgggc gtcttcatga tttcccagta cggctacctg 1140
 actctgaaca atgacagcca atcgggtgggt cgttcctctt tctactgcct ggaatatctc 1200
 ccttctcaaa tgctgagaac gggcaacaac ttacacctca gctacacctt cgaggacgtt 1260
 ccttctcaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320
 gaccagtacc tgattacctt ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
 cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440
 ctgcctggac ctgtctccg gcaacaaga gtctccaaga cgctggatca aaacaacaac 1500
 agcaactttg ctggactgg tgccaccaa taccatctaa atggaagaaa ttcattggtt 1560
 aatcccgggtg tcgcatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620
 ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
 atgacaaatg aagaggaat tcgtcctacc aaccggtag ccaccgagga atacgggact 1740
 gttagcagca acctgcaggc ggctaact gtagccaga cacaagttgt caacaaccag 1800
 ggagccttac ctggtatggg ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860
 gccaagattc ctcacacgga cggcaacttt caccctctc cgctgatggg cggcttttga 1920
 ctgaagcatc cgctctctca gatcctgatc aaaaacactc ctgttcttgc taatcccccg 1980
 gaggtgttta cgctgccaa gtttgcctt ttcacacac agtacagcac cggccaggtc 2040
 agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa ccagagatt 2100
 cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccaggg 2160
 gtttattctg agcctcgccc cattgggtact cgttacctca cccgtaatct gtaa 2214

<210> 34
 <211> 2214
 <212> DNA
 <213> new AAV serotype, clone rh.44

<400> 34
 atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
 gagtgggtgg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctgcgac 240
 cagcggctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaagg gaccggtaga accgtcacct cagcgttccc ccgactctc cacgggcatc 480
 ggcaagaagc gccagcagcc cgctagaag agactgaact ttgggcagac tggcgactca 540
 gagtcagtcc ccgacctca accaatcggg gaaccaccag caggccccctc tggctctggga 600
 tctggtacaa tggctgcagg cgggtggcgca ccaatggctg acaataacga gggcgccgac 660
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcacccgaac ctgggctttg cccacctaca acaatcacct ctacaagcaa 780
 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

```

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960
cagggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020
acgggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080
cagggtctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140
actctgaaca atggcagcca atcggtgggg cgttcctctt tctactgcct ggaatatttc 1200
ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacggt 1260
cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttata 1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440
ctgcctggac cttgtctccg gcaacaaga gtctccaaga cgctggatca aaacaacaac 1500
agcaactttg cttggactgg tgccaccaa taccatctaa atggaagaaa ttcattgggt 1560
aatcccggtg tcgcatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc 1620
ggagtcttga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact 1740
gttagcagca acctgcaggc ggctaact gcagcccaga cacaagttgt caacaaccag 1800
ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccactctg 1860
gccaaagattc ctcacacgga cggcaacttt caccgtctc cgctgatggg cggctttgga 1920
ctgaagcatc cgctcctca gatcctgatc aaaaacatc ctgttcctgc taatcccccg 1980
gagggtgtta cgctgcaa gtttcttct ttcacacac agtacagcac cggccagggtc 2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt 2100
cagtatacct ccaattttga cgaacagact ggtgtggact ttgccgttga cagccagggt 2160
gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

```

```

<210> 35
<211> 2214
<212> DNA
<213> new AAV serotype, clone rh.65

```

```

<400> 35
atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtggtagg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctgggtgt tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcgacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagaac gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540
gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggcttgga 600
tctggtacaa tggctgcagg cggtagcgct ccaatggcag acaataacga aggcgccgac 660
ggagtgggta atgctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc 840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960
cagggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020
acgggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080
cagggtctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

```

```

" acTctgaacā atggcagcca atcgggtgggt cgttctctt tctactgcct ggaatatttc 1200
ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260
cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttattc 1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440
ctgcctagac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500
agcaactttg cttggactgg tgccacaaa taccatctaa atggaagaaa ttcattgggtt 1560
aatcccgggtg tcgcatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc 1620
ggagtctga tttttgaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
atgacaaatg aagaggaaat tcgtctacc aaccggtag ccaccgagga atacgggact 1740
gttagcagca acctgcaggc ggctaact gacgcccaga cacaagttgt caacaaccag 1800
ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860
gccaaagttc ctacacgga cggcaactt caccgtctc cgctgatggg cggctttgga 1920
ctgaagcatc cgctcctca gatcctgac aaaaacactc ctgttctgc taatcccccg 1980
gaggtgttta cgctgcaa gtttgttct ttcacacac agtacagcac cgccagggtc 2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt 2100
cagtatacct ccaattttga caaacaga ct ggtgtggact ttgccgttga cagccagggt 2160
gtttattctg agcctcgccc cattgggtact cgttacctca cccgtaatct gtaa 2214

```

```

<210> 36
<211> 2214
<212> DNA
<213> new AAV serotype, clone rh.67

```

```

<400> 36
atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgaca ggcttacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accatgcca cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcctccag 360
gccaagaagc gggttctcga acctctcggc ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540
gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggcttgga 600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgcgac 660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaa cttgggctttg cccacctaca acaaccacct ctacaagcaa 780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc 840
tggggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960
caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa cttaccagc 1020
acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080
cagggctgcc tgctccgtt cccggcgagc gtcttcatga tccccagta cggctacctg 1140
actctgaaca atggcagcca atcgggtggg cgttctctt tctactgcct ggaatatttc 1200
ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260
cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttattc 1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

```

```

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500
agcaactttg cttggactgg tgccacaaa taccatctaa atggaagaaa ttcatgggtt 1560
aatcccgggtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc 1620
ggagtcttga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact 1740
gttagcagca acctgcaggc ggctaact gcagcccaga cacaagttgt caacaaccag 1800
ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860
gccaagattc ctcacacgga cggcaacttt caccgctctc cgctgatggg cggctttgga 1920
ctgaagcatc cgcctcctca gatcctgac aaaaacactc ctgttcctgc taatcccccg 1980
gagggtgtta cgcctgcaa gtttgcttct ttcacacac agtacagcac cggccagggtc 2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt 2100
cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160
gtttattctg agcctcgccc cattggtact cgttacctca cccgtaattc gtaa 2214

```

```

<210> 37
<211> 2214
<212> DNA
<213> new AAV serotype, clone rh.55

```

```

<400> 37
atggctgccc atggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtgtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgtgtgt tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgaca ggcttacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccgtacca cagcgttccc ccgactctc cacgggcatc 480
ggcaagaag gccagcagcc cgccagaag agactcaatt tcggtcagac tggcgactca 540
gagtcagtc ccgacctca acctatcgga gaacctccag cagcgcctc tagtgtggga 600
tctgttaca tggtgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660
ggagtgggta gttcctcggg aaattggcat tgcgattcca cacggctggg cgacagagtc 720
atcaccacca gcaccggac ctgggctttg ccacctaca acaaccacct ctacaagcaa 780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
ctcatcaaca acaactggg attccggccc aagaagctca acttcaagct gttcaacatc 960
cagggtcaag aggtcacaac gaatgacggc gtcacgacca tcgccataa ccttaccagc 1020
acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080
cagggtgcc tgcttcggt cccggcggac gtcttcatga tccccagta cggctacctg 1140
actctgaaca atggcagcca atcgggtggg cgttcctctt tctactgcct ggaatatttc 1200
ccttctcaaa tgctgagaac gggcaacaac ttcacctca gctacacct cgaggacgtt 1260
cccttcacac gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttata 1320
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440
ctgcctggac cttgcttccg gcaacgaaga gtctccaaga cgctggatca aaacaacaac 1500
agcaactttg cttggactgg tgccacaaa taccatctaa atggaagaaa ttcatgggtt 1560
aatcccgggtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccttcgagc 1620
ggagtcttga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact 1740

```

gttagcagca	atctgcaggc	ggctaacact	gcagcccaga	cacaagttgt	caacaaccag	1800
ggagccttac	ctggtatggt	ctggcagaac	cgggacgtgt	acctgcaggg	tcccatctgg	1860
gccaaagattc	ctcacacgga	cggcaacttt	caccgcgtctc	cgctgatggg	cggcttttggg	1920
ctgaagcatc	cgcctctcta	gatcctgata	aaaaaacttc	ctgttcctgc	taatcccccg	1980
gaggtgttta	cgcctgccaa	gtttgcttct	ttcatcacac	agtacagcac	cggccagggtc	2040
agcgtggaga	tcgagtggga	gctgcagaag	gagaacagca	agcgttgga	cccagagatt	2100
cagtatacct	ccaattttga	caaacagact	ggtgtggact	ttgccgttga	cagccaggggt	2160
gtttattctg	agcctcgccc	cattggtact	cgttacctca	cccgtaatct	gtaa	2214

<210> 38
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.47

<400> 38	atggctgccc	atggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	60
	gagtgggtgg	acctgaaacc	tggagccccc	aaacccaaag	ccaaccagca	aaagcaggac	120
	gacggccggg	gtctggtgct	tcctggctac	aagcacctcg	gaccttcaa	cggactcgac	180
	aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	agcacgacaa	ggcctacgac	240
	cagcagctca	aagcgggtga	caatccgtac	ctgcggtata	atcacgctga	cgccgagttt	300
	caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	tcgggagcgc	agtcttcag	360
	gccaaagaag	gggttctcga	acctctcggg	ctggttgagg	aaggcgctaa	gacggctcct	420
	ggaaagaaga	gaccggtaga	gccgtcacca	cagcgttccc	ccgactcctc	cacgggcatac	480
	ggcaagaaag	gccagcagcc	cgcagaaag	agactcaatt	tcggtcagac	tggcgactca	540
	gagtcagtc	ccgacctcta	acctatcgga	gaacctccag	cagcgccctc	tagtgtggga	600
	tctggtacaa	tggctgcagg	cgggtggcga	ccaatggcag	acaataacga	aggtgccgac	660
	ggagtgggta	gttctctcgg	aaattggcat	tgcgattcca	catggctggg	cgacagagtc	720
	atcaccacca	gcacccgaac	ctggggccctg	cccacctaca	acaaccacct	ctacaagcaa	780
	atctccaacg	ggacctcggg	aggcagcacc	aacgacaaca	cctactttgg	ctacagcacc	840
	ccctgggggt	attttgactt	taacagattc	cactgccact	tctcaccacg	tgactggcag	900
	cgactcatca	acaacaactg	gggattccgg	cccaagagac	tcagcttcaa	gctcttcaac	960
	atccagggtca	aagaggtcac	gcagaatgaa	ggcaccaaga	ccatcgccaa	taaccttacc	1020
	agcacgggtc	aggtcttttc	ggactcggaa	taccagctgc	cctacgtcct	cggctccgca	1080
	caccagggct	gcctgcctcc	gttcccggcg	gacgtcttca	tgattcccca	gtacggctac	1140
	ctgactctga	acaatggcag	ccaatcgggtg	ggtcgttctt	ctttctactg	cctggaatat	1200
	ttcccttctc	aatgtctgag	aacgggcaac	aacttcacct	tcagctacac	cttcgaggac	1260
	gttcccttcc	acagcagcta	cgcacacagc	cagagcctgg	accggctgat	gaatcctctt	1320
	atcgaccagt	acctgtatta	cctggccaga	acacagagca	acgcaggagg	cacagctggc	1380
	aatcgggaac	tgcagtttta	tcagggcggg	cctaccacca	tggccgaaca	agccaaaaac	1440
	tggctgcctg	gaccttgctt	ccggcaacaa	agagtctcca	agacgctgga	tcaaaacaac	1500
	aacagcaact	ttgcttggac	tgggtgccacc	aaataccatc	taaatggaag	aaattcattg	1560
	gttaatcccc	gtgtcgccat	ggcaaccac	aaggacgacg	aggaacgctt	cttcccttcg	1620
	agcggagtc	tgattttttg	aaaaactgga	gcagctaata	agactacact	ggaaaatgtg	1680
	ttaatgacaa	atgaagagga	aattcgtcct	accaaccggg	tagccaccga	ggaatacggg	1740
	actgttagca	gcaacctgca	ggcggctaac	actgcagccc	agacacaagt	tgtcaacaac	1800
	cagggagcct	tacctggtat	ggtctggcag	aaccgggacg	tgtacctgca	gggtcccatc	1860
	tgggccaaga	ttcctcacac	ggacggcaac	tttcaccgt	ctccgctgat	gggcggcttt	1920
	ggactgaagc	atccgcctcc	tcagatcctg	atcaaaaaca	ctcctgttcc	tgctaattccc	1980
	ccggagggtgt	ttacgcctgc	caagtttgct	tctttcatca	cacagtacag	caccggccag	2040

gtcagcgtgg agatcagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100
 attcagtata cctccaattt tgacaaacag actggtgtgg actttgccgt tgacagccag 2160
 ggtgtttatt ctgagcctcg ccccatgggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 39
 <211> 2214
 <212> DNA
 <213> new AAV serotype, clone rh.69

<400> 39
 atggctgctg acggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
 gagtgggtgg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaag gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac 480
 ggcaagaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540
 gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccccctc tggcttgga 600
 tctggtacaa tggctgcagg cggtggcgcc ccaatggcag acaataacga aggcgcgac 660
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780
 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840
 tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
 ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960
 caggtcaagg aggtcacac gaatgacggc gtcacgacca tcgccataa ccttaccagc 1020
 acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080
 cagggctgcc tgccctcgtt cccggcgagc gtcttcatga ttccccagta cggctacctg 1140
 actctgaaca atggcagcca atcggtggtg cgttcctctt tctactgcct ggaatatctc 1200
 cctttctaaa tgctgagaac gggcaacaac ttcaccatca gctacacctt cgaggacgtt 1260
 cccttccaca gcagctacgc acacagccag agcctggacc ggtgatgaa tcctcttattc 1320
 gaccagtacc tgattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
 caggaaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440
 ctgcctggac ctgtcttcg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500
 agcaactttg ctggactgg tgccacaaa taccatctaa atggaagaaa ttcatgtgtt 1560
 aatcccgggt tcgccatggc aaccacaaag gacgacgagg aacgcttctt cccttcgagc 1620
 ggagtcctga tttttgaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680
 atgacaaatg aagaggaaat tcgtcctacc aaccggtag ccaccgagga atacgggact 1740
 gttagcagca acctgcaggc ggctaactc gcagcccaga cacaagttgt caacaaccag 1800
 ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860
 gccaaagatt ctacacaga tggcaacttt caccgctctc ctttaatggg cggttttgga 1920
 cttaaactc cgctcctca gatcctcatc aaaaactc ctgttcctgc ggatcctcca 1980
 acagcgttca accaggccaa gctgaattct ttcacacgc agtacagcac cgacaagtc 2040
 agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa ccagagatt 2100
 cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgaggg 2160
 gtttactctg agcctcgccc cattggcact cgttacctca cccgtaactc gtaa 2214

<210> 40
 <211> 2214
 <212> DNA

<213> new AAV serotype, clone rh.54

<400> 40

```

atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc      60
gagtgggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca gaagcaggac      120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac      180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct      420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480
ggcaagaagc gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca      540
gagtcagtcc ccgacctca acctctcgga gaaccaccag caggccccctc tggcttgga      600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgcgcgac      660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720
atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa      780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct cttcaacatc      960
caagtcaagg aggtcacgac gaatgacggc gtcacgacca tcgctaataa ccttaccagc     1020
acggttcagg tcttttcgga ctcgagtagc cagctgccgt acgtcctcgg ctctgcccac     1080
cagggctgcc tgctccggtt cccggcggac gtcttcatga ttctcagta cggctacctg     1140
actctgaaca atggcagcca atcggtgga cgttcacctt tctactgcct ggaatacttc     1200
ccttctcagg tgctgagaac gggtaacaac ttcaccttca gttacacctt cgaggacgtg     1260
cctttccaca gcagctacgc gcacagccag agcctagacc ggctgatgaa tccccctatc     1320
gaccagtacc tgtattacct ggctagaaca cagagtaacc caggaggcac atctggcaat     1380
cgggaactgc agttttacca gggcgggcct tccacctagg ccgaacaagc caagaactgg     1440
ttacctggac ctgtctcccg gcaacaaaga gtttccaaaa cactggatca aaacaacaac     1500
agcaactttg ctggactgg tgccaccaa tatcacctga acggcagaaa ctcatgtgtg     1560
aatcctggtg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc     1620
ggagtcctga tttttggaaa aactggagca accaacaaga ctacattgga aaacgtgtta     1680
atgacaaatg aagaagaaat tcgtcctact aatcctgtgg ccacagaaga atacgggata     1740
gtcagcagca atttacaagc ggccaatact gcagcccaga cacaagttgt caacaaccag     1800
ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg     1860
gccaaaattc ctcacacaga cggcaacttt caccgtctc cgctgatggg cggcttttga     1920
ctgaagcatc cgcctctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg     1980
gaggtgttta cgcctgccaa gtttgcttct ttcacacac agtacagcac cggccagggtc     2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt     2100
cagtatacct ccaattttga caaacagaat ggtgtggact ttgccgttga cagccagggt     2160
gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa         2214

```

<210> 41

<211> 2214

<212> DNA

<213> new AAV serotype, clone rh.45

<400> 41

```

atggctgctg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc      60
gagtgggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac      180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

```


cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac 480
 ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540
 gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggctctggga 600
 tctggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgcgcgac 660
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcaccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780
 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc 840
 tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
 ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960
 caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020
 acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080
 cagggtcgcc tgcctccgtt cccggcggac gtcttcatga ttctcagta cggtacctg 1140
 actctcaaca acggtagtca ggcgtggga cgttctcct tctactgcct ggagtacttc 1200
 cctctcaga tgctgagaac gggcaacaac ttttccttca gctacacttt cgaggacgtg 1260
 cctttccaca gcagctacgc gcacagccag agtttgga ggcgtgatga tctctcatc 1320
 gaccagtacc tgtactacct gtcaagaacc cagtctacgg gaggcacagc gggaaccag 1380
 cagttgctgt tttctcaggc cgggcctagc aacatgtcga ctcaggccag aaactggctg 1440
 cctggaccct gctacagaca gcagcgcgtc tccacgacac tgtcgcaaaa caacaacagc 1500
 aactttgcct ggactggtgc caccaagtat catctgaacg gcagagactc tctggtgaat 1560
 ccgggcgtcg ccattggcaac caacaaggac gacgaggacc gcttcttccc atccagcggc 1620
 atcctcatgt ttggcaagca gggagctgga aaagacaacg tggactatag caacgtgatg 1680
 ctaaccagcg aggaagaaat caagaccacc aaccccgtag ccacagaaca gtatggcgtg 1740
 gtggctgata acctacagca gcaaaacacc gctcctattg tgggggcccgt caacagccag 1800
 ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatttgg 1860
 gccaaagattc ctacacaga tggcaacttt caccgtctc ctttaatggg cggttttggga 1920
 cttaaacatc cgcctcctca gatccttacc aaaaacactc ctgttcctgc ggatcctcca 1980
 acagcgttca accaggccaa gctgaattct ttcacacgc agtacagcac cggacaagtc 2040
 agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt 2100
 cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgaggg 2160
 gcttactctg agcctcgccc cattggcact cgttacctca cccgtaactc gtaa 2214

<210> 42
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone rh.59

<400> 42
 atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cgactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac 480
 ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc cccgacctca accaatcggga gaaccaccag caggccccctc tggctctggga 600
 tcttggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac 660
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780
 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840
 tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900
 ctcatacaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960
 cagggtcaagg aggtcacaaac gaatgacggc gtcacgacca tcgccaataa ccctaccagc 1020
 acggttcagg tcttttcgga ctcggaatac cagctgcctt acgtcctcgg ctccgcacac 1080
 cagggtgccc tgcctccgtt cccggcgagc gtcttcatga tccccagta cggctacctg 1140
 actctgaaca atggcagcca atcggtgggg cgcttctctt tctactgcct ggaatatctt 1200
 ccttctcaaa tgcctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260
 cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320
 gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380
 cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440
 ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500
 agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctgggtg 1560
 aatccgggagc tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620
 ggcaccttca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680
 atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740
 gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc 1800
 caggggagcct tacctggcat ggtctggcag aaccgggagc tgtacctgca gggctctatt 1860
 tggggccaaga ttcctcacac agatggcaac tttcacccgt ctctttaaag gggcggtctt 1920
 ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct 1980
 ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgagctacag caccggacaa 2040
 gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100
 attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160
 ggtgtttact ctgagcctcg ccccatggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 43
 <211> 2211
 <212> DNA
 <213> new AAV serotype, clone rh.43

<400> 43
 atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
 gacggccggg gcctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
 aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
 ggaaagaaga gaccagtaga gcagtcacc ccaagaaccag actcctcctc gggcatcggc 480
 aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540
 tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600
 aatacaatgg ctgcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
 gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780
 tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

```

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900
ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960
cagggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccataa cctcaccagc 1020
accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080
cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140
acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200
ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260
cctttccaca gcagctacgc ccacagccag agcttgacc ggctgatgaa tcctctgatt 1320
gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380
actctgggct tcagccaagg tgggcctaata caaatggcca atcaggcaaa gaactggctg 1440
ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500
aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaata 1560
cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttccc agtaacggga 1620
tcctgttttt ggcaacaaaa tgctgccaga gacaatgcgg attacagcga tgcatgctc 1680
accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740
gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800
gccttaccgg gtatggtctg gcagaaccgg gacgtgtacc tgcaggggcc catctggggc 1860
aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggagg ctttggcctg 1920
aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980
accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040
gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100
tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160
tactctgaac cccgcccacat tggcaccctg tacctcacc gtaatctgta a 2211

```

```

<210> 44
<211> 2211
<212> DNA
<213> new AAV serotype, clone hu.3

```

```

<400> 44
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgcgg cctggtttga ggaacctgt taagacggct 420
ccgggaaaaa agaggccggg agagcactct cctgtggagc cagactcctc ctcgggaacc 480
ggaaaagcgg gccagcagcc tgcaagaaaa agattaaatt ttggtcagac tggagacgca 540
gactccgtac ctgaccccca gcctctcggg cagccaccag cagccccctc tggctctggg 600
tctactacaa tggctacagg cagtggcgca ccaatggcag acaataacga gggtgccgat 660
ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctgga cgacagagtc 720
atcgccacca gcaccgaa cctgggccctg cccacataca acaaccacct ctacaagcaa 780
atctccagcc aatcaggagc ctgcaacgac aaccactact ttggctacag cccccctgg 840
gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900
atcaacagca actggggatt ccggcccaaa agactcaact tcaagctctt taatattcaa 960
gtcaaagagg tcacgcagaa tgacggtagc acgacgattg ccaataacct taccagcacg 1020
gttcagggtg ttactgactc ggagtaccag ctcccgtacg tcccgggctc ggcgcaccaa 1080
ggatgcctcc cgccgtttcc agcggacgtc ttcatggtcc cacagtatgg atacctcacc 1140

```

ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt actgcctgga gtactttcct 1200
 tctcagatgc tgcgtactgg aaacaacttt cagttcagct acacttttga agacgtgcct 1260
 ttccacagca gctacgctca ctgccagagt ctggatcggc tgatgaatcc tctgatcgac 1320
 cagtacctgt attatctgaa caagacacaa acaaatagtg gaactcttca gcagtctcgg 1380
 ctactgttta gccaagctgg accaaccaac atgtctcttc aagctaaaaa ctggctgcct 1440
 ggaccttgct acagacagca gcgtctgtca aaacaggcaa acgacaataa caactgcaac 1500
 tttccctgga ctgcagctac aaagtatcat ctaaattggcc gggactcgtt ggtaaatcca 1560
 ggaccagcta tggccagtca caaggatgac gaagaaaagt ttttcccat gcatggaacc 1620
 ctgatatttg gtaaacaagg aacaaatgcc aacgacgcgg atttggaataa tgcacatgatt 1680
 acagatgaag aagaaatcag gccccaat cccgtggcta cggagcagta cgggactgtg 1740
 tcaataaatt tgcaaaactc aaacactggc ccaactacag gaactgtcaa tcaccaagga 1800
 gcgttacctg gtatggtgtg gcaggatcga gacgtgtacc tgcagggacc catttgggcc 1860
 aagattcctc acaccgatgg acactttcat cttctccac tgatgggagg ttttggactc 1920
 aaacaccgcg ctctcagat catgatcaa agcactccg ttcagccaa tcctccaca 1980
 aacttcagtt ctgccaagtt tgcttcttcc atcacacagt attccacggg acaggtcagc 2040
 gtggagatcg agtgggagct gcagaaggag aacagcaaac gctggaatcc cgaaattcag 2100
 tacacttcca actacaacaa gtctgttaat gtggacttta ctgtggacac taatggtgtg 2160
 tattcagagc ctgcacctat tggcaccaga tacctgactc gtaattctgta a 2211

<210> 45
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.5

<400> 45
 atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggccacca ccacaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcttacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcagagttt 300
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcgaaaaaga ggggtcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctctc gggaaccgga 480
 aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct 600
 actacaatgg ctacaggcag tggcgacca atggcagaca ataacgagg tgccgatgga 660
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaattc 780
 tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
 tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960
 aaagagggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
 cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080
 tgcctcccgc cgtttccagc ggacgtcttc atgggtccac agtatggata cctcacctg 1140
 aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct 1200
 cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260
 cacagcagct acgtcacag ccagagctct gatcggctga tgaatcctct gatcgaccag 1320
 tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380
 ctgttttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

```

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagtcgcaa ggatgacgaa gaaaagtfff tccccatgca tggaaacctg 1620
atatttggtg aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680
gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740
aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980
ttcagttctg ccaagtttgc ttttttcatc acacagtatt ccacgggaca ggtcagcggtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 46
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.1

```

```

<400> 46
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaaac tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcttgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcttacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctcctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtccagactg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctctg tctgggatct 600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaata 780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaaaaaga ctcaacttca agctctttaa tattcaagtc 960
aaagagggtc cgcagaatgg cggtagcagc acgattgcca ataaccttac cagcacgggt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080
tgctctccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcggg aggacgctct tccttttact gcctggagta ctttcttct 1200
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260
cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320
tacctgtatt atctgaacaa gacacaaaac aatagtggaa ctcttcagca gtctcggcta 1380
ctgttttagc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg gcaacaacaa cagcaacttt 1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagtcacaa ggatgacgaa gaaaagtfff tccccatgca tggaaacctg 1620
atatttggtg aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680
gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

```

```

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaaag 1860
attcctcaca ccgatggaca ctttcatcct tctccactga cgggaggttt tggactcaaa 1920
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 47
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.4

```

```

<400> 47
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgtc tcttgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctctc gggaaccgga 480
aaagcggggc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggatct 600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660
gtgggttaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
accaccagca ccggaacctg ggccctgccc acatacaaca accacctcta caagcaaatt 780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccaactgccac ttttaccac gtgactggca aagactcgtc 900
aacaacaacc ggggattccg gcccaaaaaga ctcaacttca agctctttaa tattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgcc aataacctac cagcacggtt 1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080
tgctctccgc cgtttccagc ggacgtcttc atggctccac agtatggata cctcacctg 1140
aacaacggga gtcaggcggg aggacgtctt tctttttact gcctggagta ctttcttctt 1200
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260
cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320
tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380
ctgttttagc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagtcacaa ggatgacgaa gaaaagtgtt tccccatgca tggaaacctg 1620
atatttggtg aacaagggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680
gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740
aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaaag 1860
attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

```

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
 acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 48
 <211> 2209
 <212> DNA
 <213> new AAV serotype, clone hu.2

<400> 48
 atggctgccc atggttatcc tccagattgg ctgaggaca ctctctctga agggataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcttacgac 240
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgagagttt 300
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
 aaagcgggcc agcggcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540
 tccgtacctg acccccagcc tctcgacag ccaccagcag cccctctgg tctgggatct 600
 actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatac 780
 tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
 tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg gccccaaaaga ctcaacttca agctctttaa tattcaagtc 960
 aaagagggtca cgcagaatga cggtagacg acgattgccg ataaccttac cagcacggtt 1020
 cagggtgttta ctgactcga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080
 tgctctccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcacctg 1140
 aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttctt 1200
 cagatgtctg gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260
 cacagcagct acgtcacag ccagagtctg gatcggtgga tgaatcctct gatcgaccag 1320
 tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380
 ctgttttagc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440
 ccttgctaca gacagcagc tctgtcaaaa caggcaaagc acaacaacaa cagcaacttt 1500
 ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
 ccagctatgg ccagtcacaa ggatgacgaa gaaaagtgtt tccccatgca tggaaacctg 1620
 atatttggtg aacaaggaa aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680
 gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtagcg gactgtgtca 1740
 aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatcg ccaaggagcg 1800
 ttacctggtg tgggtgtggc ggatcgagac gtgtacctg agggacccat ttgggccaag 1860
 attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920
 caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980
 ttcagtctcg ccaagtgttc tcttttcatc acacagtatt ccacgggaca ggtcagcgtg 2040
 gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
 acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2209

<210> 49
 <211> 2208

212 DNA

<213> new AAV serotype, clone hu.25

<400> 49

```

atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga    60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac    120
ggcagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac    180
aagggagagc cggcacaaga ggcagacgcc gcggccctcg agcacgaca ggcttacgac    240
cggcagctca acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt    300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag    360
gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg    420
ggaaaaaaga gaccggtaga gcaactctct gcggagccag actcctcttc gggaaccgga    480
aaagcggggc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac    540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct    600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga    660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcata    720
accacaagca ctgaacctg ggccctgccc acctacaaca accacctcta caagcaaata    780
tccagccaat caggagcctc aaacgacaac cactattttg gctacagcac cccttggggg    840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcata    900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc    960
aaagaggtca cgcagaatga cggtagcag acgattgccg ataaccttac cagcacgggt    1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga    1080
tgctctccgc cgttcccagc ggacgtcttc atggtcccac agtatggata cctcaccctg    1140
aacaacggga gtcaggcggg aggacgctct cccttttact gcctggagta ctttcttct    1200
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc    1260
cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag    1320
tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta    1380
ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg gctgcctgga    1440
ccttgctaca gacagcagc tctgtcaaag caggcaaagc acaacaacaa cagcaacttt    1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga    1560
ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaacctg    1620
atatttggtg aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca    1680
gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtagcg gactgtgtca    1740
aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg    1800
ttacctggta tgggtgtgga ggcagcagat gtgtaccttc agggacccat ttgggccaag    1860
attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa    1920
cacccgcctc ctcagattat gatcaaaaac actcccgttc cagccaatcc tcctacaaac    1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg    2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac    2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacaataa tggcgtgtac    2160
tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaa    2208

```

<210> 50

<211> 2208

<212> DNA

<213> new AAV serotype, clone hu.15

<400> 50

```

atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga    60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac    120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactctac    180

```



```

aagggagagc'cggtcgcgga ggacagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga gggttcttga acctctgggc ttggttgagg agcctgttaa aacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
aaagcgggca accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct 600
actacaatgg ctacaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcata 720
accaccagca cccgaacctg ggctctgccc acctacaata accacctcta caagcaaata 780
tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccaactgccac ttttcaccac gtgaccggca aagactcata 900
aacaacaact ggggattccg accaaaaaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgcc aataaccttac cagcacgggt 1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggcttggc gcatcaagga 1080
tgctctccgc cgctccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcggg aggcagctct tccttttact gcctggagta ctttcttctt 1200
cagatgtctg gtactggaaa caactttcag ttcagctaca ctttgaaga cgctccttct 1260
cacagcagct acgttcacag ccagagctcg gatcggctga tgaatcctct gatcgaccag 1320
tacctgtatt atctgaacaa gacacaatca aatagtgga ctcttcagca gtctcggcta 1380
ctgttttagc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagc tctgtcaag caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tggaaacctg 1620
atatgttgta aacaaggaa aaatgctaac gacgcggatt tggacaatgt catgattaca 1680
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtagcg atatgtgtca 1740
aataatttgc aaaactcaaa tacttgtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtgga ggatcgagac gtgtacctg agggacccat ttgggccaag 1860
attcctcaca ccgatggaca ctttcatcct tctccactta tgggaggttt tggactcaaa 1920
caccacctc ctcagatcat gattaaaaac actcccgctc cagccaatcc tcccacaaac 1980
ttcagttctg ccaagtgtgc ttctttcatc acacagtatt ccacgggaca agtcagcgtg 2040
gagatcgagt gggagctgca gaaggaggac agcaaacgct ggaaccccg gatccagtac 2100
acttccaact ataacaacac tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 51
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.16

```

```

<400> 51
atggctgccc atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgtgga agctcaaac tggccacca ccgcaaagc ccgagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctg gacccttcaa cggactctac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga gggttcttga acctctgggc ttggttgagg agcctgttaa aacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

```

'aaagcgggca' accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct 600
 actacaatgg ctacaggcag tggcgaccca gtggcagaca ataacgaggg tgccgatgga 660
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
 accaccagca cccgaacctg ggctctgccc acctacaaca accacctcta caagcaaatac 780
 tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840
 tattttgact tcaacagatt cacttgccac ttttcaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg accaaagaga ctcaacttca agctctttaa cattcaagtc 960
 aaagagggtca cgcagaatga cggtagcagc acgattgccca ataactttac cagcacgggt 1020
 cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgccctcccg cgttcccgagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggga gtcaggcggg aggacgctct tccttttact ggctggagta ctttcttct 1200
 cagatgctgc gtactggaaa caactttcag ttcagctaca ctttgaaga cgttctttc 1260
 cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320
 tacctgtatt atctgaacaa gacacaatca aatagtggaa cccttcagca gtctcggcta 1380
 ctgttttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440
 ccttgctaca gacagcagcg tctgtcaaa caggcaaacg acaacaacaa cagcaacttt 1500
 ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
 ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620
 atatttggtg aacaaggaaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680
 gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtagcg atatgtgtca 1740
 aataatttgc aagactcaaa tactgggtcca actactggaa ctgtcaatca ccaaggagcg 1800
 ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
 attcctcaca ccgatggaca ctttcatcct tctccactta tgggaggttt tggactcaaa 1920
 caccacctc ctcagatcat gattaaaaac actcccggtc cagccaatcc tcccacaaac 1980
 ttcagttctg ccaagtttgc tttttctc acacagtatt ccacgggaca agtcagcgta 2040
 gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccgga gatccagtac 2100
 acttccaact ataacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
 tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 52
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.18

<400> 52
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaac tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtacctg gaccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
 cggcagctcg aaagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420
 ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctcctc gggaaccgga 480
 aaagcgggcc agcagcctgc gagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct 600
 actacaatgg ctacaggcag tggcgaccca gtggcagaca ataacgaggg tgccgatgga 660
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatac 780

```

tccagtcctaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacagct ggggattccg acccaaaaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggta cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
caagtgttta ccgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080
tgctcccg cgttccagc agacgtcttt atggtccac agtatggata cctcacctg 1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct 1200
cagatgtgc gtactggaaa caactttcag ttcagctaca ctttgaaga cgttcccttc 1260
cacagcagct acgtcacag ccagagtctg gatcggtgc tgaatcctct gatcgaccag 1320
tacctatatt atctgaacaa gacacaatca aatagtggaa ctcttcagca gtctcggcta 1380
ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagc tctgtcaaag caggcaaacy acaacaaca cagcaacttt 1500
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tggaaacctg 1620
atatttggtg aacaaggaa aaatgctaac gacgcggatt tggacaatgt catgattaca 1680
gatgaagaag aaatccgcac caccaatccc gtggtacgg agcagtacgg atatgtgtca 1740
aataatttgc aaaactcaaa tactgggtca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtgga ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcctcaca cggacgggca ctttcatcct tctccactaa tgggaggttt tgggtcaaa 1920
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcctacaaac 1980
ttcagttctt ccaagtgtgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtat 2100
acttccaact acaacaaatc tgtaatgtg gactttactg tggacactaa tgggtgtgat 2160
tcagagcctc gccccattgg caccagatag ccgactcgta atctgtaa 2208

```

```

<210> 53
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.8

```

```

<400> 53
atggctgccc atggttatct tccagattgg ctgaggaca ctctctctga aggaacaaga 60
cagtgggtga agctcaaacc tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcttgggtac aagtacctcg gaccttcaa cggactcgac 180
aaggggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcttacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagtgt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctct gcggagccag actcctctc gggaaccgga 480
aaagcggggc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg accccagacc tctcgacag ccaccagcag cccctctgg tttgggatct 600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgcgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggca cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780
tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggta cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080

```

```

||tgcttccgc cgtttccagc ggacgtcttc atggtccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct 1200
cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260
cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320
tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta 1380
ctgttttagtc aagctggacc caccagcatg tcttttcaag ctaaaaactg gctacctgga 1440
ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cggctacaaa gtaccaccta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaacctg 1620
atatttggtg aacaaggaa aaatgctaac gacgcggatt tggacaatgt catgattaca 1680
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtagcg atatgtgtca 1740
aataatttgc aaaactcaaa tacttggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggca tgggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980
ttcagtctcg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

<210> 54
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone rh.56

```

<400> 54
atggctgctg atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggccaccca ccaccaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgtc tcctgggtac aagtacctcg gacccttcaa cggaactcgac 180
aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcgagttt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480
aaagcggggc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg ttgggatct 600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cttcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
accaccagca cccgaacctg ggcccagccc acctacaaca accacctcta caagcaaac 780
tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggtca cgcagaatga cggtagcag acgattgcca ataaccttac cagcacggtt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080
tgctcccgc cgtttccagc ggacgtcttc atggtccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct 1200
cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260
cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320
tacctgtatt atctgaacaa aacacaatca aatagtggag ctcttcagca gtctcggcta 1380

```

ctgttttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440
 ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500
 ccctggactg cgggtacaaa gtaccaccta aatggccggg actcgttggg taatccagga 1560
 ccagctatgg ccagtcacaa agacgatgaa gaaaagtgtt tccccatgca tggaaacctg 1620
 atatattggt aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680
 gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740
 aataatttgc aaaactcaaa tactgggtcca actactggaa ctgtcaatca ccgaggagcg 1800
 ttacctggca tgggtgtgga ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
 attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920
 caccgcctc ctcagatcat gatcaaaaac actcccgctc cagccaatcc tcccacaaac 1980
 ttcagtctcg ccaagtgttc tcttttcac acacagtatt ccacggggca ggtagcgtg 2040
 gagatcgagt gggagctgca gaaagagaac agcaaagcgt ggaatcccga aattcagtag 2100
 acttccaact acaacaatc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 55
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.7

<400> 55
 atggctgccg atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
 cagtgggtga agctcaaac tggccacca ccaccaagc ccgagagcg gcataaggac 120
 gacagcaggg gtcttgtgtc tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg gacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gcaactcctc gcggagccag actcctcctc gggaaccgga 480
 aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tttgggatct 600
 actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660
 gtgggtaatt cctcaggaaa ttggcattgc gattccaat ggctgggcga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780
 tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840
 tattttgact tcaacagatt ccaactgccac ttttaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
 aaagaggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
 cagggtttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080
 tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcacctg 1140
 aacaacggga gtcaggcggg aggacgctct tccttttact gcctggagta ctttccttct 1200
 cagatgcttc gtactggaaa caactttcag ttcagctaca ctttgaaga cgttcctttc 1260
 cacagcagct acgctcacag ccagagtctg gatcggtga tgaatcctct gatcgaccag 1320
 tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta 1380
 ctgttttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440
 ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500
 ccctggactg cgggtacaaa gtatcaccta aatggccggg actcgttggg taatccagga 1560
 ccagctatgg ccagtcacaa agacgatgaa gaaaagtgtt tccccatgca tggaaacctg 1620
 atatattggt aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaaagaa	aaatccgcac	caccaatccc	gtggctacgg	agcagtacgg	atatgtgtca	1740
aataatttgc	aaaactcaaa	tactggtcca	actactggaa	ctgtcaatca	ccaaggagcg	1800
ttacctggca	tgggtgtggca	ggatcgagac	gtgtacctgc	agggacccat	ttgggccaag	1860
attcctcaca	ccgatggaca	ctttcatcct	tctccactga	tgggaggttt	tgggctcaaa	1920
cacccgcctc	ctcagatcat	gatcaaaaac	actcccgttc	cagccaatcc	tcccacaaac	1980
ttcagttctg	ccaagtttgc	ttctttcatc	acacagtatt	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaagagaac	agcaaacgct	ggaatcccga	aattcagtag	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	tggacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 56
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.10

<400> 56						
atggctgccc	atggttatct	tccagattgg	ctcgaggaca	ctctctctga	aggaataaga	60
cagtgggtga	agctcaaacc	tggcccacca	ccaccaaagc	tcgcagagcg	gcatcaggac	120
gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gaccttcaa	cggactcgac	180
aaaggagagc	cggctcaacga	ggcagacgac	gcggccctcg	agcacgacaa	ggcctacgac	240
cggcagctcg	acagcggaga	caaccctgac	ctcaagtaca	accacgccga	cgcggagttt	300
caggagcgtc	ttaaagaaga	tacgtctttt	gggggaacc	tcggacgagc	agtcttcag	360
gcgaaaaaga	gggttcttga	acctctgggc	ctggttgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
aaggcggggc	atcagcctgc	gagaaagaga	ttgaattttg	gtcagactgg	agacgcagac	540
tccgtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccacaag	tctgggatct	600
actacaatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgaggg	tgccgatgga	660
gtgggtaatt	cctcaggaaa	ttggcattgc	gattcccaat	ggctgggcga	cagagtcata	720
accaccagca	cccgaacctg	ggccctgccc	acctacaaca	accacctcta	caagcaaata	780
tccagccaat	caggagcctc	gaacgacaac	cactactttg	gctacagcac	cccctggggg	840
tattttgact	tcaacagatt	ccactgtcac	ttctccccac	gtgattggca	aagactcata	900
aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttaa	cattcaagtc	960
aaagagggtca	cgcagaatga	cggtagcagc	acgattgccca	ataaccttac	cagcacgggt	1020
cagggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgctctccgc	cgtttccagc	ggacgtcttc	acgggtcccac	agtattggata	cctcaccctg	1140
aacaacggga	gtcagcggtt	aggacgctct	tccttttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtactggaaa	caaccttacc	ttcagctaca	cctttgagga	cgttcctttc	1260
cacagcagct	acgctcacag	ccagagtttg	gaccggctga	tgaatcctct	gatcgaccag	1320
tatctatatt	atctgaacag	gacacaatca	aatagtggaa	ctcttcagca	gtctaggcta	1380
ctgttttagcc	aagctggacc	caccagcatg	tctcttcaag	ctaaaaactg	gctgcctgga	1440
ccttgctaca	gacagcagcg	tctttcaaag	caggcaaacg	acaacaacaa	cagcaacttt	1500
ccctggactg	cggctacaaa	gtatcatcta	aatggccggg	actcgttggg	taatccagga	1560
ccagctatgg	ccagccacaa	agacgatgaa	gaaaagtgtt	tccccatgca	tgggaaccctg	1620
atatttggtg	aacaagggaac	aaatgctaac	gacgcggatt	tggagcatgt	tatgattaca	1680
gatgaagaag	aaatcaggac	caccaatcct	gtggctacag	agcagtacgg	aaacgtgtca	1740
aataatttgc	aaaactcaaa	tactggtcca	actacagaaa	atgtcaatca	ccaggggagcg	1800
ttacctggta	tgggtgtggca	ggatcgagac	gtgtacctgc	agggacccat	ttgggccaag	1860
attcctcaca	ccgacggaca	ctttcaccct	tctccactga	tgggaggttt	tggactcaaa	1920
cacccgcctc	ctcaaatcat	gatcaaaaac	actcccgttc	cagccaatcc	tcccacaaac	1980

tacagttctg	ccaagtttgc	ttctttcatc	acacagtatt	ccacgggcca	ggtcagcgtg	2040
gagattgagt	gggagctgcg	gaaggagaac	agcaaacgct	ggaaccccga	gatccagtat	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	tggacactaa	tggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgttaa		2208

<210> 57
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.11

<400> 57						
atggctgccg	atggttatct	tccagattgg	ctcgaggaca	ctctctctga	aggaataaga	60
cagtgggtgga	agctcaaacc	tggccacca	ccaccaaagc	ccgcagagcg	gcatcaggac	120
gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gaccttcaa	cggactcgac	180
aaaggagagc	cggccaacga	ggcagacgcc	gcggccctcg	agcacgacaa	ggcctacgac	240
cggcagctcg	acagcggaga	caaccctgac	ctcaagtaca	accacgccga	cgcggagttt	300
caggagcgtc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttcag	360
gcgaaaaaga	gggttcttga	acctctgggc	ctggttgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
aaagcgggcc	atcagcctgc	gagaaagaga	ttgaattttg	gtcagactgg	agacgcagac	540
tccgtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccacaag	tttgggatct	600
actacaatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgaggg	tgccgatgga	660
gtgggtaatt	cctcaggaaa	ttggcattgc	gattcccaat	ggctgggcga	cagagtcata	720
accaccagca	cccgaacctg	ggccctgccc	acctacaaca	accacctcta	caagcaaata	780
tccagccaat	caggagcctc	gaacgacaac	cactactttg	gctacagcac	cccctggggg	840
tattttgact	tcaacagatt	ccactgtcac	ttctccccac	gtgattggca	aagactcata	900
aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttaa	cattcaagtc	960
aaggaggtca	cgcagaatga	cggtagcagc	acgattgcca	ataaccttac	cagcacggtt	1020
cagggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgccctccgc	cgtttccagc	ggacgtcttc	atggtcccac	agtatggata	cctcaccctg	1140
aacaacggga	gtcaggcggt	aggacgtctt	tccttttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtactggaaa	caactttacc	ttcagctaca	cctttgagga	cgttcctttc	1260
cacagcagct	acgttcacag	ccagagtttg	gaccggctga	tgaatcctct	gatcgaccag	1320
tatctatat	atctgaacag	gacacaatca	aatagtggaa	ctcttcagca	gtctaggcta	1380
ctgttttagc	aagctggacc	caccagcatg	tctcttcaag	ctaaaaactg	gctgcctgga	1440
ccttgctaca	gacagcagcg	tccttcaaag	caggcaaacg	acaacaacaa	cagcaacttt	1500
ccctggactg	cggctacaaa	gtatcgtcta	aatggccggg	actcgttggg	taatccagga	1560
ccagctatgg	ccagccacaa	agacgatgaa	gaaaagtgtt	tccccatgca	tggaaccctg	1620
atattttgga	aacaagggaac	aatgctaac	gacgcggatt	tggagcatgt	tatgattaca	1680
gatgaagaag	aaatcaggac	caccaatcct	gtggctacag	agcagtacgg	aaacgtgtca	1740
aataatttgc	aaaactcaaa	tactgggtcca	actacagaaa	atgtcaatca	ccaggagcgg	1800
ttacctggta	tggtgtggca	ggatcgagac	gtgtacctgc	agggacccat	ttgggccaag	1860
attcctcaca	ccgacggaca	ctttcaccct	tctccactga	tgggaggttt	tggactcaaa	1920
caccgcctc	ctcaaatcat	gatcaaaaac	actcccgttc	cagccaatcc	tcccacaac	1980
ttcagttctg	ccaagtttgc	ttctttcatc	acacagtatt	ccacgggcca	ggtcagcgtg	2040
gagattgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaaccccga	gatccagtat	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	tggacactaa	tggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgttaa		2208

<210> 58

<211> 2208

<212> DNA

<213> new AAV serotype, clone hu.9

<400> 58

```

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga    60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac    120
aacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac    180
aaaggagagc cgtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac    240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagtgt    300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag    360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg    420
ggaaaaaaga ggccggtaga gactctctct gtggagccag actctctctc gggaaccgga    480
aaagcggggc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac    540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct    600
actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga    660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatt    720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaattc    780
tccagccaat caggagcctc gaacgacaac cactactttg gctgcagcac cccctggggg    840
tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc    900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc    960
aaagagggtc cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt   1020
cagggtgttta ctgactcggg gtacccgctc ccgtacgtcc tcggctcggc gcatcaagga   1080
tgctctccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg   1140
aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttctt   1200
cagatgtctg gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc   1260
cacagcagct acgtcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag   1320
tatctatatc atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta   1380
ctgttttagc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga   1440
ccttgctaca gacagcagc tctttcaagc caggcaaagc acaacaacaa cagcaacttt   1500
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga   1560
ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaaccctg   1620
atatattggt aacaaggaa aaatgctaac gacgcggatt tggagcatgt tatgattaca   1680
gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtagcg aaacgtgtca   1740
aataatttgc aaaactcaaa tactgggtcca actacagaaa atgtcaatca ccaggagcgc   1800
ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag   1860
attcctcata ccgacggaca ctttcacctt tctccactga tgggaggttt tggactcaaa   1920
caccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac   1980
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg   2040
gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat   2100
acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat   2160
tcagagcctt gccccattgg caccagatac ctgactcgta atctgtaa                    2208

```

<210> 59

<211> 2208

<212> DNA

<213> new AAV serotype, clone hu.12

<400> 59

```

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga    60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac    120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac    180

```



```

aaaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcttc ggggaaccgga 480
aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct 600
actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatac 780
tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgtcac ttctcccccac gtgattggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggtca cgcagaatga cgttacgacg acgattgcca ataaccttac cagcacggtt 1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgctctccgc cgtttccagc ggacgtcttc atggtccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcggg aggacgccct tccttttact gcctggagta ctttcttctc 1200
cagatgtctg gtactggaaa caactttacc ttcagctaca cctttgagga cgttctcttc 1260
cacagcagct acgtcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320
tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380
ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagcg tctttcaag caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagccacaa agacgatgaa gaaaagtgtt tccccatgca tgggaccctg 1620
atatttggtg aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680
gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740
aataatttgc aaaactcaaa tactgggtcca actacagaaa atgtcaatca ccagggagcg 1800
ttacctggtg tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcttcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920
caccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980
ttcagtctcg ccaagtgtgc tcttttcac acacagtatt ccacgggcca ggtcagcgtg 2040
gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 60
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.23

```

```

<400> 60
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcttc ggggaaccgga 480

```

```

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatac gatgg cttcaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctgcaaca accatctgta caagcaaatac 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggatttccg gccaagaga ctgagcttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt 1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgccctccgc cgttcccgag agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggca gtcaggcggg aggagctctt tccttttact gcctggagta ttttccttct 1200
cagatgcttc gtaccggaaa caactttacc ttacgttaca cctttgaaga cgttcccttc 1260
catagcagct acgtccacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctgaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgattac 1500
tcgtggactg gagtaccaca gtaccacctc aatggaagag actctctggt gaatccgggc 1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620
atcttttgaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tttgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
acctacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
cttccaggca tggctcggca ggacagagac gtgtacctgc gggggcccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt tggacttaaa 1920
caccctctc cacaattct catcaagaac accccggtag ctgcgaatcc ttcgaccact 1980
ttcagtgcgg caaagtctgc ttccttcac acacagtact ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtag 2100
acttccaact acaacaatac tgtaaatgtg gactttactg tggacactaa tgggtgtgat 2160
tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaa 2208

```

<210> 61
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.26

```

<400> 61
atggctgccc atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtgga agtcaaacc tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cggatcaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcaactctct gcggagccag actcctcctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatac gatgg cttcaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatac 780

```

```

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gccaagaga ctgagcttca agctctttaa cattcaagtc 960
aaagaggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cgttcccgag agacgtcttc atgggtgccac agtatggata cctcaccctg 1140
aacaacggca gtcaggcggg aggacgctct tccttttact gcctggagta ctttccttct 1200
cagatgcttc gtaccggaaa caactttacc ttacgtctaca cctttgaaga cgttccttct 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccagat gtccaggctt 1380
cagttttctc aggcgggagc aagtgcatt cgggaccagt ctgaaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgtattac 1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttctcagag cgggggtctc 1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
cttcaggga tggctggga ggacagagac gtgtacctgc agggggccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa 1920
caccctctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacggggca ggtagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 62
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.19

```

```

<400> 62
atggctgccg atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaac tggcccacca ccaccaagc ccgagagcg gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcttacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaagaaga tacgtctttt ggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggagaaaaga ggccggtaga gactctctct gcggagccag actctctctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaagaga ttgaattttg gccagactgg agacgcagac 540
tcagtacctg accccagacc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacgtatg cttcaggcag tggcgacca atggcagaca ataacgaggg cggcgacgga 660
gtgggtaatt cctcgggaaa ttggtattgc gattccacat ggtggggcga cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gccaagaga ctgagcttca agctctttaa cattcaagtc 960
aaagaggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

```

```

tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggca gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct 1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380
cagttttctc aggcgggagc aagtgcattt cgggaccagt ctagaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgtattac 1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cgggggttctc 1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tttgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
cttcagggca tggctctggc ggacagagac gtgtacctgc agggggccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctctg tgggcggatt cggacttaaa 1920
caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980
ttcagtgcgg caaagtctgc ttccttcctc acacagtact ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccg aattcagtac 2100
acttccaact acaacaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 63
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.20

```

```

<400> 63
atggctgccg atggttatct tccagattgg ctccaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaac tggcccacca ccaccaaac cgcagagcg gcataaggac 120
gacagcaggg gtctgtgtct tcctgggtac aggtacctcg gacccttcaa cggactcgac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgtcga cgcggagttt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa ggcggctccg 420
ggagaaaaga ggccggtaga gactctctc gcggagccag actcctctc ggaaccgga 480
aaagcgggcc agcagcctgc aagaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacagatg cttcaggcag tggcgacca atggcagaca ataacgagg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgcacctg ggcctgccc acctacaaca accatctgta caagcaaact 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
cattttgact tcaacagatt cactgcccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaagaga ctacgttca agctctttaa cattcaagtc 960
aaagagggtc cgcagaatga cggtagcag acgattgcca ataaccttac cagcacggtt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggca gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct 1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

```

cagttttctc aggccggagc aagtgcattt cgggaccagt ctagaaactg gcttcctgga 1440
 ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgtattac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560
 ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cgggggttctc 1620
 atcttttgaa aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgtattaca 1680
 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggt 1800
 cttccaggca tggctctggca ggacagagac gtgtacctgc agggggcccat ctgggcaaaag 1860
 attccacaca cggacggaca ttttcacccc tctcccccca tgggcgggatt cggacttaaa 1920
 caccctcttc cacaatttct catcaagaac accccgggtac ctgcgaatcc ttcgaccact 1980
 ttcagtgcgg caaagtttgc ttccttcctc acacagtact ccacggggca ggtcagcggtg 2040
 gagatcaggt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtag 2100
 acttccaact acaacaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
 tcagagcctc gcccatttgg cgccagatac ctgactcgta atctgtaa 2208

<210> 64
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.27

<400> 64
 atggctgccg atggttatct tccagattgg ctgcaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaac tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aaggagagcg cggctcaacga ggcagacgac gcggccctcg agcacgacaa ggcctacgac 240
 cggcagctcg acagcggaga caaccggtac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gactctctct gcggagccag actctctctc gggaaccgga 480
 aaagcgggac agcagcctgc aagaagaga ttgaattttg gtcagactgg agacgcagac 540
 tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctctg tctgggaact 600
 aatacagatg cttcaggcag tggcgacca atggcagaca ataacgaggc gcccgacgga 660
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggtatggcga cagagtcac 720
 accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaact 780
 tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
 tatttcgact tcaacagatt cactgcccac ttctccccac gtgactggca aagactcatc 900
 aacaacaact ggggatttcc gcccaagaga ctgagcttca agctctttta cattcaagtc 960
 aaagagggtc cgcagaatga cggtagcagc acgattgcca ataaccctac cagcacgggt 1020
 cagggtgtta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaaggga 1080
 tgccttccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggca gtcaggcggg aggacgctct tccttttact gcctggagta ctttcttctc 1200
 cagatgcttc gtaccggaac caactttacc ttcagctaca cctttgaaga cgttcttctc 1260
 catagcagct acgctcacgg ccaaagctcg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgat gtccaggctt 1380
 cagttttctc aggccggagc aagtgcattt cgggaccagt ctagaaactg gcttcctgga 1440
 ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgtattac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560
 ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cgggggttctc 1620
 gtcttttgaa aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgtattaca 1680

```

gacgaagagg aaatcaggac caccaatccc gcggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggt 1800
cttcaggca tggctctggca ggacagagac gtgtacctgc agggggcccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa 1920
caccctctc cacaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980
ttcagtgcgg caaagtgtgt ttccttcac acacagtact ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttcaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 65
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.21

```

```

<400> 65
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga 60
cagtggtgga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac 120
gacagcaggg gtcttctgtct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aaggagagag cggctcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga taaccctgac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccgcc tctcggacag ccaccagcag cccctcttg tctgggaact 600
aatagatgg cttcaggcag tggcgacca atggcagaca ataacgagg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaact 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt cactgccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgcc ataaccttac cagcacgggt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgctctccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggca gtcaggcggt aggacgtct tccttttact gcctggagta ctttcttct 1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca ctttgaaga cgttccttct 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaact ccaagcggaa ccaccagat gtccaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctgaaactg gcttcttga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgttac 1500
tcgtggactg gagctacca gtaccacctc aatggaagag actctctggt gaatccgggc 1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttctcagag cggggttctc 1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tatgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggt 1800
cttcaggca tggctctggca ggacagagac gtgtacctgc agggggcccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa 1920
caccctctc cacaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

```

ttcagtgctg	caaagtttgc	ttccttcac	acacagtact	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	aattcagtag	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	tggaactaa	tggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 66
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.24

<400> 66						
atggctgccc	atggttatct	tccagattgg	ctcaggaca	ccctctctga	aggaataaga	60
cagtgggtgga	agctcaaacc	tggtccacca	ccaccaaagc	ccgcagagcg	gcataaggac	120
gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gaccttcaa	cggactcgac	180
aagggagagc	cggctaacga	ggcagacgcc	gcggccctcg	agcacgacaa	ggcctacgac	240
cggcagctcg	acagcggaga	taaccctgac	ctcaagtaca	accacgccga	cgcggagttt	300
caggagcgcc	ttaaagagga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcaaaaaaga	ggattcttga	acctctgggc	ctggttgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gcggagccag	actcctctc	gggaaccgga	480
aaagcggggc	agcagcctgc	aagaaagaga	ttgaattttg	gtcagactgg	agacgcagac	540
tcagtacctg	acccccggcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggaact	600
aatacgatgg	cttcaggcag	tggtcgacca	atggcagaca	ataacgaggg	cggcgacgga	660
gtgggttaatt	cctcgggaaa	ttggcattgc	gattccacat	ggatgggcga	cagagtcac	720
accaccagca	cccgacctg	ggccctgccc	acctacaaca	accatctgta	caagcaaatc	780
tccagccagt	ctggagccag	caacgacaac	caactctttg	gctacagcac	ccccctgggg	840
tattttgact	tcaacagatt	ccactgccac	ttctccccac	gtgactggca	aagactcatc	900
aacaacaact	ggggattccg	gccaagaga	ctcagcttca	agctctttaa	cattcaagtc	960
aaagagggtca	cgcagaatga	cgttacgacg	acgattgcc	ataaccttac	cagcacggtt	1020
caggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgcttccccg	cgttccccag	agacgtcttc	atggtgccac	agtatggata	cctcaccttg	1140
aacaacggca	gtcaggcggg	aggacgtctt	tccttttact	gcctggagta	ctttcttctt	1200
cagatgcttc	gtaccggaaa	caactttacc	ttcagctaca	cctttgaaga	cgttcttttc	1260
catagcagct	acgttcacag	ccaaagtctg	gaccgtctca	tgaatcctct	catcgaccag	1320
tacctgtatt	acttgagcag	aacaaacact	ccaagcggaa	ccaccacgat	gtccaggctt	1380
cagttttctc	aggccggagc	aagtgcattt	cgggaccagt	ctagaaactg	gcttcctgga	1440
ccctgttacc	gccagcagcg	agtatcaaag	acagctgcgg	acaacaaca	cagtgattac	1500
tcgtggactg	gagctacca	gtaccacctc	aatggaagag	actctctggt	gaatccgggc	1560
ccagctatgg	ccagccacaa	ggacgatgaa	gaaaaatatt	ttcctcagag	cggggttctc	1620
atctttggaa	aacaagactc	gggaaaaact	aatgtggaca	ttgaaaaggt	tatgattaca	1680
gacgaagagg	aaatcaggac	caccaatccc	gtggctacgg	agcagtatgg	ttctgtatct	1740
accaacctcc	agagcggcaa	cacacaagca	gtacctcag	atgtcaacac	acaaggcgtt	1800
cttccaggca	tggtctggca	ggacagagac	gtgtacctgc	agggggccat	ctgggcaaa	1860
attccacaca	cggacggaca	ttttcaccct	tctccccctc	tgggcggatt	cggacttaaa	1920
caccctctc	cacaaattct	catcaagaac	accccggtac	ctgcgaatcc	ttcgaccact	1980
ttcagtgctg	caaagtttgc	ttccttcac	acacagtact	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	aattcagtag	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	tggaactaa	tggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 67
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.22

<400> 67
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttggtgt tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
 aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggccctacgac 240
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgcc ttaaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480
 aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540
 tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
 aatacgtatg ctacaggcag tggcgacca atggcagaca ataacgaggg cgcgcagcga 660
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggagg cagagtcac 720
 accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaattc 780
 tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
 tattttgact tcaacagatt ccactgccac ttctcccccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg gcccaagaga ctgagcttca agctctttaa cattcaagtc 960
 aaagaggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
 cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgccctccgc cgttcccgag agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggca gtcaggcggg aggcagctct tccttttact gcctggagta ctttcttctc 1200
 cagacgcttc gtaccggaaa caactttacc ttacagtaca cctttgaaga cgttcctttc 1260
 catagcagct acgtcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcag acaaaact ccaagcggaa ccaccagat gtccaggctt 1380
 cagttttctc aggcgggagc aagtgcatt cgggaccagt ctagaaactg gcttcctgga 1440
 ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgtattac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560
 ccagctatgg ccagccaca ggacgatgaa gaaaaatatt ttctcagag cgggggttctc 1620
 atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tatgattaca 1680
 gacgaagagg aatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
 cttccaggca tgggtctggca ggacagagac gtgtacctgc agggggcccat ctgggcaaa 1860
 attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920
 caccctctc cacaattct catcaagaac accccggtag ctgcgaatcc ttcgaccact 1980
 ttcagtgcgg caaagtgtgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040
 gagatcgagt gggagctgca gaaggagaac agcaaagcgt ggaatcccga aattcagtac 2100
 acttccaact acaacaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 68
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.28

<400> 68
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga aactcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

"gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcaaaaaaga gggttctgga acctctgagc ctggttgagg agcctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gactctccc gcagagccag attcctctc cggactgga 480
 aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctcg tctgggaact 600
 aatacgtagg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgcgcagcga 660
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggca cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780
 tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840
 tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
 aaagaggcca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
 cagggtgtta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgcctcccg cgttcccgag agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggga gtcaggcagt aggacgtctt tcattttact gcctagagta ctttcttct 1200
 cagatgtcgc gtaccggaaa caactttacc tttagctaca cttttgagga cgttcttct 1260
 cacagcagct acgtcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccagca gtccaggctt 1380
 cagttttctc aggccggagc gaggtagatt caggaccagt ctaggaaactg gcttcttga 1440
 ccctgttacc gtcagcagcg agtatcaaag acatctgagg ataacaaca cagtgaatac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccggc 1560
 ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttctcagag cggggttctt 1620
 atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaagg catgattaca 1680
 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagcggcaa cacacaagca gctaccgag atgtcaacac acaaggcgtt 1800
 cttccaggca tggtcgggca agacagagac gtgtacctgc aggggcctac ttgggcaaa 1860
 attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaa 1920
 caccctctc cacagattct catcaagaac accccggtag ctgcgaatcc ttcgaccacc 1980
 ttcagtgcgg caaagtgtgc ttcttctatt acacagtact ccacggggca ggtcagcgtg 2040
 gagatcaggt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100
 acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
 tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 69
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.29

<400> 69
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggccacca ccacaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt 300
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcaaaaaaga gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

```

ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480
aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780
tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccaactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgcc aataacctac cagcacgggt 1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cgttcccagc agacgtcttc atgggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctagggta ctttcttctt 1200
cagatgctgc gtaccgaaa caactttacc ttcagctaca ctttgagga cgttcctttc 1260
cacagcagct acgtcacag ccagagtttg gaccgtctca tgaatcctt catcgaccag 1320
tacctgtatt acttgagcag acaaacact ccaagcgga ccaccagca gtccaggctt 1380
cagttttctc aggccggagc gagtgcatt cgggaccagt ctaggaactg gcttcttggg 1440
ccctgttacc gtcagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cggggttctt 1620
atctttggga agcaaggccc agagaaaaca aatgtggata ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctaccgag atgtcaacac acaaggcggt 1800
cttcaggga tggctcggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaa 1920
caccctctc cacagattct catcaagaac accccgttac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtgtgc ttccttcatt acacagtact ccacggggca ggtagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatccga gatccagtac 2100
acttccaact acaacaagtc tgtaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 70
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.30

```

```

<400> 70
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgtgga agctcaaacc tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttggtgt tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgcca cgcgaggttt 300
caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcaaaaaaga gggttctgga acctctgggc ctgggtgagg agcctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480
aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720

```

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780
 tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840
 tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
 aaagaggta cgcagaatga cggtagcagc acgattgccataaaccttac cagcacggtt 1020
 cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgccctcccg cgttcccgagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggga gtcaggcagt aggacgctct tcattttact gcctagagta ctttccttct 1200
 cagatgctgc gtaccggaaa cagctttacc ttcagctaca ctttgaggga cgttcctttc 1260
 cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcag aacaacaact ccaagcggaa ccaccacgca gtccaggctt 1380
 cagttttctc aggcgggagc gaggacatt cgggaccagt ctaggaaactg gcttcctgga 1440
 ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
 ccggccatgg ccagccacaa agacgatgaa gaaaagttct ttcctcagag cggggttctt 1620
 atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaagg catgattaca 1680
 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800
 cttccaggca tggctctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860
 attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt tggacttaa 1920
 caccctctc cagagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
 ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040
 gagatcaggt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100
 acttccaact aacaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
 tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaa 2208

<210> 71
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.13

<400> 71
 atggctgccg atggttatct tccagattgg ctccaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaac tggccaccca ccaccaaac cgcagagcg gcataaggac 120
 gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgcc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420
 ggaaaaaaga ggccggtaga gactctcct gcggagccag actcctcctc gggaaccgga 480
 aaagcgggc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
 aatacagtg cttcaggcag tggcgacca atggcagaca ataacgagg cgccgacgga 660
 gtgggttaatt cctcgggaaa ttggcattgc gattccacat ggtggggcga cagagtcac 720
 accaccagca cccgaacttg ggccctgccc acctacaaca accatctcta caagcaaatc 780
 tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840
 tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg gcccgaagaga ctcaacttca agctctttaa cattcaagtc 960
 aaagaggta cgcagaatga cggtagcagc acgattgccataaaccttac cagcacggtt 1020

caggtgttta	ctgactcggg	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgcctcccg	cggtccagc	agacgtcttc	atggtgccac	agtatggata	cctcaccctg	1140
aacaacggga	gtcaggcagt	aggacgtctc	tcattttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtaccggaaa	caactttacc	ttcagctaca	cctttgagga	cgttcctttc	1260
cacagcagct	acgctcacag	ccagagtctg	gaccgtctca	tgaatcctct	catcgaccag	1320
tacctgtatt	acttgagcag	aacaaacact	ccaagcggaa	ccaccacgca	gtccaggcctt	1380
cagttttctc	aggccggagc	aagtgcatt	cgggaccagt	ctaggaactg	gcttcctgga	1440
ccctgttacc	gccagcagcg	agtatcaaag	acatctgcgg	ataacaacaa	cagtgaatac	1500
tcgtggactg	gagctaccaa	gtaccacctc	aatggcagag	actctctggt	gaatccgggc	1560
ccggccatgg	ccagccacaa	ggacgatgaa	gaaaagtgtt	ttcctcagag	cggggttctc	1620
atctttggga	agcaaggctc	agagaaaaca	aatgtggaca	ttgaaaagg	catgattaca	1680
gacgaagagg	aaatcaggac	caccaatccc	gtggctacgg	agcagtatgg	ttctgtatct	1740
accaacctgc	agggcggcaa	cacacaagca	gctaccgcag	atgtcaacac	acaaggcgtt	1800
cttcaggga	tggtctggca	ggacagagac	gtgtacctgc	aggggcccat	ctgggcaaa	1860
attccacaca	cggacggaca	ttttcacccc	tctccctca	tgggcggatt	cggacttaa	1920
cacctcctc	cacagattct	catcaagaac	accccggtac	ctgcgaatcc	ttcgaccacc	1980
ttcagtgcgg	caaagtgtgc	ttctttcatc	acacagtatt	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	gatccagtac	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	ttgacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 72
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.34

<400> 72						
atggctgccc	atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60					
cagcgggtgga	agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120					
gacagcaggg	gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180					
aagggagagc	cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240					
cggcagctcg	acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagtgt 300					
caggagcgcc	ttaaagaaga tacgtccttt gggggcaacc tcggacgagc agtcttccag 360					
gcgaaaaaga	gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420					
ggaaaaaaga	ggccggtaga gactctctct gtggagccag actcctcctc gggaaccgga 480					
aaggcgggcc	agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540					
tcagtacctg	acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600					
aatacgatgg	ctacaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga 660					
gtgggtaatt	cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720					
accaccagca	cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780					
tccagccaat	caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840					
tattttgact	tcaacagatt cactgcccac ttttcaccac gtgactggca aagactcatc 900					
aacaacaact	ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960					
aaagagggtca	cgagaatga cggtagcagc acgattgccataaaccttac cagcacgggt 1020					
caggtgttta	ctgactcggg	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgcctcccg	cggtccagc	agacgtcttc	atggtgccac	agtatggata	cctcaccctg	1140
aacaacgaga	gtcaggcagt	aggacgtctc	tcattttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtaccggaaa	caactttacc	ttcagctaca	cctttgagga	cgttcctttc	1260
cacagcagct	acgctcacag	ccagagtctg	ggccgtctca	tgaatcctct	catcgaccag	1320

tacctgtatt	acttgagcag	aacaaacact	ccaagtggaa	ccaccacgca	gtcaaggctt	1380
cagttttctc	aggccggagc	gagtgacatt	cgggaccagt	ctaggaactg	gcttcctgga	1440
ccctgttacc	gccagcagcg	agtatcaaag	acatctgcgg	ataacaacaa	cagtgaatac	1500
tcgtggactg	gagctaccaa	gtaccacctc	aatggcagag	actctctggt	gaatccgggc	1560
ccggccatgg	caagccacaa	ggacgatgaa	gaaaagtttt	ttcctcagag	cgggggttctc	1620
atctttggga	agcaaggctc	agagaaaaca	aatgtggaca	ttgaaaaggt	catgattaca	1680
gacgaagagg	aaatcaggac	aaccaatccc	gtggctacgg	agcagtatgg	ttctgtatct	1740
accaacctcc	agagaggcaa	cagacaagca	gctaccgcag	atgtcaacac	acaaggcggt	1800
cttccaggca	tggcttgcca	ggacagagat	gtgtaccttc	agggggcccat	ctgggcaaag	1860
attccacaca	cggacggaca	ttttcacccc	tctccctca	tgggtggatt	cggacttaaa	1920
cacctctctc	cacagattct	catcaagaac	accccggtac	ctgcgaatcc	ttcgaccacc	1980
ttcagtgcgg	caaagtttgc	ttccttcctc	acacagtact	ccacgggaca	ggtcagcggt	2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	aattcagtac	2100
acttccaact	acaacaagtc	tgttaatgtg	gactttactg	tggacactaa	tggcgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 73
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.35

<400> 73						
atggctgccc	atggttatct	tccagattgg	ctcgaggaca	ctctctctga	aggaataaga	60
cagcggtgga	agctcaaacc	tggcccacca	ccaccagagc	ccgcagagcg	gcataaggac	120
gacagcaggg	gtcttggtct	tcctgggtac	aagtacctcg	gaccttcaa	cggactcgac	180
aaggagagc	cggctcaacga	ggcagacgcc	gcggccctcg	agcacgacaa	agcctacgac	240
cggcagctcg	acagcggaga	caaccctgac	ctcaagtaca	accacgccga	cgcggagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcgaaaaaga	gggtacttga	acctctgggc	ctggttgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
aaggcgggccc	agcagcctgc	aagaaaaaga	ttgaattttg	gtcagactgg	agacgcagac	540
tcagtacctg	acccccagcc	tctcgacag	ccaccagcag	ccccctctgg	tctgggaact	600
aatacgatgg	ctacaggcag	tggcgacca	atggcagaca	ataacgaggg	cgccgacgga	660
gtgggtaatt	cctcgggaaa	ttggcattgc	gattccacat	ggatgggcga	cagagtcac	720
accaccagca	cccgaacctg	ggccctgccc	acctacaaca	accacctcta	caaacaatt	780
tccagccaat	caggagcctc	gaacgacaat	cactactttg	gctacagcac	cccttggggg	840
tattttgact	tcaacagatt	ccactgccac	ttttcaccac	gtgactggca	aagactcatc	900
aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttaa	cattcaagtc	960
aaagagggtca	cgcagaatga	cggtagcagc	acgattgcca	ataaccttac	cagcacgggt	1020
cagggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgcctcccgc	cgttcccagc	agacgtcttc	atggtagcac	agtatggata	cctcaccctg	1140
aacaacggga	gtcaggcagt	aggacgtctt	tcattttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtaccggaaa	caactttacc	ttcagctaca	cttttgagga	cgttcctttc	1260
cacagcagct	acgtcacag	ccagagtctg	ggccgtctca	tgaatcctct	catcgaccag	1320
tacctgtatt	acttgagcag	aacaaacact	ccaagtggaa	ccaccacgca	gtcaaggctt	1380
cagttttctc	aggccggagc	gagtgacatt	cgggaccagt	ctaggaactg	gcttcctgga	1440
ccctgttacc	gccagcagcg	agtatcaaag	acatctgcgg	ataacaacaa	cagtgaatac	1500
tcgtggactg	gagctaccaa	gtaccacctc	aatggcagag	actctctggt	gaatccgggc	1560
ccggccatgg	caagccacaa	ggacgatgaa	gaaaagtttt	ttcctcagag	cgggggttctc	1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcggt 1800
cttccaggca tggctctggca ggacagagat gtgtaccttc agggggcccat ctgggcaaaag 1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920
caccctcctc cacagattct catcaagaac accccggtag ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtgtgc ttccttcctc acacagtact ccacgggaca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggaagaa agcaaagcgt ggaatcccga aattcagtag 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgtg atctgtaa 2208

<210> 74
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.36

<400> 74
atggctgccc atggttatct tccagattgg ctgcaggaca ctctctctga aggaataaga 60
cagcgggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggagagc cggctaacga ggacagcgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggtagctga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctcctc gggaaccgga 480
aagggcgggc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacgtagg ctacaggcag tggcgacca atggcagaca ataacgaggg cgcggacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcctc 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtc cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcttcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcagc aggacgtctt tcattttact gcctggagta ctttccttct 1200
cagatgtctg gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260
cacagcagct acgtcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380
cagttttctc aggcgggagc gagtgcatt cgggaccagt ctaggaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg caagccacaa ggacgatgaa gaaaagtgtt ttcctcagag cgggggttctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcggt 1800
cttccaggca tggctctggca ggacagagat gtgtaccttc agggggcccat ctgggcaaaag 1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc	catcaagaac	accccggtac	ctgcgaatcc	ttcgaccacc	1980
ttcagtgctg	caaagtttgc	ttccttcac	acacagtact	ccacgggaca	2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	2100
acttccaact	acaacaagtc	cgtaaatgtg	gactttactg	tggacactaa	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa	2208

<210> 75
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.33

<400> 75					
atggctgccc	atggttatct	tccagattgg	ctcaggagaca	ctctctctga	aggaataaga 60
cagcgggtgga	agctcaaacc	tggcccacca	ccaccagagc	ccgcagagcg	gcataaggac 120
gacagcaggg	gtcttgctgt	tcctgggtac	aagtacctcg	gaccttcaa	cggaactcgac 180
aagggagagc	cggtcaacga	ggcagacgcc	gcggccctcg	agcacgaca	agcctacgac 240
cggcagctcg	acagcggaga	caacccgtac	ctcaagtaca	accacgccga	cgcggaagttt 300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcctccag 360
gcgaaaaaga	gggtacttga	acctctgggc	ctggttgagg	aacctgttaa	gacggctccg 420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga 480
aaggcgggcc	agcagcctgc	aagaaaaaga	ttgaattttg	gtcagactgg	agacgcagac 540
tcagtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggaact 600
aatacagtg	ctacaggcag	tggcgacca	atggcagaca	ataacgagg	cgccgacgga 660
gtgggtaatt	cctcgggaaa	ttggcattgc	gattccacat	ggatgggcga	cagagtcac 720
accaccagca	cccgaacctg	ggccctgccc	acctacaaca	accacctcta	caaacaaatt 780
tccagccaat	caggagcctc	gaacgacaat	cactactttg	gctacagcac	cccttggggg 840
tattttgact	tcaacagatt	ccactgccac	ttttaccac	gtgactggca	aagactcatc 900
aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttaa	cattcaagtc 960
aaagagggtca	cgcagaatga	cggtacgacg	acgattgcca	ataaccttac	cggcacgggt 1020
cagggtgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga 1080
tgctctccgc	cgttccagc	agacgtcttc	atggtgccac	agtatggata	cctcacctg 1140
aacaacggga	gtcaggcagt	aggacgctct	tcattttact	gcctggagta	cttctcttct 1200
cagatgctgc	gtaccggaaa	caactttacc	ttcagctaca	cttttgagga	cgttcttttc 1260
cacagcagct	acgtcacag	ccagagtctg	ggccgtctca	tgaatcctct	catcgaccag 1320
tacctgtatt	acttgagcag	aacaaacact	ccaagtggaa	ccaccacgca	gtcaaggctt 1380
cagttttctc	aggccggagc	gagtgcatt	cgggaccagt	ctaggaactg	gcttcttgga 1440
ccctgttacc	gccagcagcg	agtatcaaag	acatctgcgg	ataacaacaa	cagtgaatac 1500
tcgtggactg	gagctaccaa	gtaccacctc	aatggcagag	actctctggt	gaatccgggc 1560
ccggccatgg	caagccacaa	ggacgatgaa	gaaaagtttt	ttcctcagag	cggggttctc 1620
atctttggga	agcaaggctc	agagaaaaca	aatgtggaca	ttgaaaaggt	catgattaca 1680
gacgaagagg	aaatcaggac	aaccaatccc	gtggctacgg	agcagtatgg	ttctgtatct 1740
accaacctcc	agagaggcaa	cagacaagca	gtaccgcag	atgtcaacac	acaaggcggt 1800
cttccaggca	tggcttgga	ggacagagat	gtgtaccttc	aggggcccat	ctgggcaaa 1860
attccacaca	cggacggaca	ttttacccc	tctccctca	tgggtggatt	cggacttaaa 1920
caccctcctc	catcaagaac	accccggtac	ctgcgaatcc	ttcgaccacc	1980
ttcagtgctg	caaagtttgc	ttccttcac	acacagtact	ccacgggaca	ggtcagcgtg 2040
gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	aattcagtac 2100
acttccaact	acaacaagtc	tgtaaatgtg	gactttactg	tggacactaa	tggcgtgtat 2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa	2208

<210> 76
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.45

<400> 76
 atggctgccc atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcatagggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
 aaggagagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgggagttt 300
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gcaactctct gtggagccag actctctctc gggaaccgga 480
 aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
 tcagtacctg acccccagcc tctcgagcag ccaccagcag cccctctctg tctgggaact 600
 aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga 660
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
 tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac ccttggggg 840
 tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
 aaagaggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
 cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cccaccctg 1140
 aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttcttct 1200
 cagatgtctg gtaccggaaa caactttacc ttcagctaca cttttgagga cgttctttc 1260
 cacagcagct acgtcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcac aacaacact ccaagtggaa ccaccacgca gtcaaggctt 1380
 cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaaactg gcttcttgg 1440
 ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccggg 1560
 ccggccgtgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620
 atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
 gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcgtt 1800
 cttccaggca tggcttgga ggacagagat gtgtaccttc aggggcccac ctgggcaaag 1860
 attccacaca cggacggaca ttttcacccc tctccctca tgggtggatt cggacttaa 1920
 caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
 ttcagtgcgg caaagtgtgc ttccttcac acacagtact ccacgggaca ggtcagcgtg 2040
 gagatcagat gggagctgca gaaggaaaac agcaaacgct ggaatccccg aattcagtac 2100
 acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160
 tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 77
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.47

<400> 77
 atggctgccc atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcatagggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
 caggagcggc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctcctc gggaaccgga 480
 aaggcggggc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
 tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
 aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatggggca cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
 tccagccaat caggagcctc gaacgacagt cactactttg gctacagcac cccttggggg 840
 tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc 900
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
 aaagaggta cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt 1020
 cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgcctcccgc cgttcccagc agacgtcttc atgggtgccac agtatggata cctcacctcg 1140
 aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttcttct 1200
 cagatgctgc gtaccgaaa caactttacc ttccagctaca cttttgagga cgttctttc 1260
 cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcac aacaacact ccaagtggaa ccaccacgca gtcaaggctc 1380
 cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaaactg gcttctctgga 1440
 ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
 ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cgggggttctc 1620
 atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggc catgattaca 1680
 gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcgtt 1800
 cttccaggca tggctctggca ggacagagat gtgtaccttc aggggcccac ctgggcaaag 1860
 attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920
 caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
 ttccagtgcg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040
 gagatcagat gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100
 acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 78
 <211> 2211
 <212> DNA
 <213> new AAV serotype, clone hu.48

<400> 78
 atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtgggtgg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120
 gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagcagc agtcttccag 360
 gccagaagc gggttctcga acctctcggc ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcttc gggcatcggc 480
 aagacaggcc agcagcccgc taaaaagaga ctcaattttg gccagactgg cgactcagag 540
 tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600
 actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
 gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcca cagagtcac 720
 accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaate 780
 tccagtactt caacgggggc cagcaacgac aaccactact tcggctacgg caccctctgg 840
 ggggtattttg atttcaacag attccactgc cacttttcac cactgtactg gcagcgactc 900
 atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960
 gtcgaggagg tcacgacgaa tgatggcgct acaaccatcg ctaataacct taccagcacg 1020
 gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080
 ggctgcctcc ctccgttccc ggcggacgtg ttcattgattc cgcaatacgg ctacctgacg 1140
 ctcaacaatg gcagccaagc cgtgggacgt tcattctttt actgcctgga atatttccct 1200
 tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggaagtgcct 1260
 ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320
 caatacctgt attacctgaa cagaacacaa aatcagtcgg gaagtgccca aaacaaggac 1380
 ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
 ggacctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500
 ttacactgga ctgggtgctt aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560
 ggcaccgctg tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgc 1620
 atgatttttg gaaaagagag cgccggagct tcaagcactg cattggacaa tgtcatgatt 1680
 acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740
 gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800
 gcattacctg gcatgggtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860
 aaaattcctc acacagatgg acactttcac ccgtctctc ttatgggcgg ctttgactc 1920
 aagaacccgc ctctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980
 gagttttcag ctacaaagtt tgcttcattc atcaccat actccacagg acaagtgagt 2040
 gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100
 tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
 tatactgagc ctgcgcccat tggcaccctg taccttacc gtccctgtga a 2211

<210> 79
 <211> 2211
 <212> DNA
 <213> new AAV serotype, clone rh.71

<400> 79
 atggctgccg atggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
 gagtgggtgg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120
 gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cgactcagac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgcgga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
 gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
 ggaagaaac gtccggtaga gcagtcgcca caagagccag actcctcttc gggcatcggc 480
 aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540
 tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600
 actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
 gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcca cagagtcac 720

```

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaadc 780
tccagtgtct caacgggggc cagcaacgac aaccactact tcggctacag cccccctgg 840
gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900
atcaacaaca attggggatt ccggcccaag agactcaact tcaaaactctt caacatccaa 960
gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020
gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080
ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140
ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgccttga atatttcctt 1200
tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260
ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320
caatacctgt attacctgaa cagaactcaa aatcagtcctg gaagtgccca aaacaaggac 1380
ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500
tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560
ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgc 1620
atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgcatgatt 1680
acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740
gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800
gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860
aaaattcctc acacagatgg acactttcac ccgtctctc ttatgggcgg ctttggactc 1920
aagaaccgc ctctcagat cctcatcaaa aacacgcctg ttcttgcaa tcctccggcg 1980
gagttttcag ctacaaagt ttgttctatt atcacccaat actccacagg acaagtgagt 2040
gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100
tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcaccgtg taccttacct gtcctctgta a 2211

```

```

<210> 80
<211> 2214
<212> DNA
<213> new AAV serotype, clone hu.43

```

```

<400> 80
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtgg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcttacgac 240
cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgcgagttt 300
caggagcgtc tgcaagaaga tacgcctttt gggggcaacc tcgggcgagc agtcttccag 360
gccagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactctc cacgggcatc 480
ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtc ccgacctca accaatcgga gaaccaccag caggccccctc tggcttggga 600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgcgac 660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcacacca gcaccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780
atctccagtg cttaacggg gccagcaac gacaaccact acttcggcta cagcaccctc 840
tgggggtatt ttgatttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900
ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960
caagtcaagg aggtcacgac gaatgatggc gtcacaacca tcgctaataa ccttaccagc 1020

```

```

acggttcaag tcttctcggg ctcggagtag cagcttccgt acgtcctcgg ctctgcgcac 1080
cagggctgcc tccctccgtt cccggcggac gtgttcataa ttcgcgaata cggctacctg 1140
acgtcaaca atggcagcca agcgtggga cgttcacatc tttactgcct ggaatatttc 1200
ccttctcaga tgctgagaac gggcaacaac tttacattca gctacacctt tgaggaagtg 1260
cctctccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa tcctctcatc 1320
gtccaatacc tgtattacct gaacagaact caaatcagt ccggaagtgc ccaaaacaag 1380
gacttgctgt tcagccgtgg gtctccagct ggcatgtctg ttcagcccaa aaactggcta 1440
cctggaccct gttatcggca gcagcgcgtt tctaaaacaa aaacagacaa caacaacagc 1500
aattttacct ggactgggtg ttaaaatat aacctcaatg ggcgtgaatc catcatcaac 1560
cctggcactg ctatggcctc acacaaagac gacgaagaca agttctttcc catgagcggg 1620
gtcatgattt ttggaaaaga gagcgccgga gcttcaaca ctgcattgga caatgtcatg 1680
attacagacg aagaggaaat taaagccact aacctgtgg ccaccgaaag atttgggacc 1740
gtggcagtc aattccagag cagcagcaca gacctgcga ccggagatgt gcatgctatg 1800
ggagcattac ctggcatggg gtggcaagat agagacgtgt acctgcaggg tcccatttgg 1860
gccaaaattc ctacacaga tggacacttt caccgtctc ctcttatggg cggcttttga 1920
ctcaagaacc cgctctca gatcctcctc aaaaacacgc ctgttctctg gaatcctccg 1980
gcggagtttt cagctacaaa gtttgcttca ttcacaccc aatactccac aggacaagtg 2040
agtgtggaaa ttgaatggga gctgcagaaa gaaacagca agcgtggaa tcccgaagtg 2100
cagtacacat ccaattatgc aaaatctgcc agcgttgatt ttactgtgga caacaatgga 2160
ctttatactg agcctcgccc cattggcacc cgttacctta cccgtcccct gtaa 2214

```

```

<210> 81
<211> 2211
<212> DNA
<213> new AAV serotype, clone hu.44

```

```

<400> 81
atggctgctg atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcagacc tggcccacca ccaccaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgtga gacggctcct 420
ggaagaagc gtccggtaga gcagtcgcca caagggccag actcctcctc gggcatcggc 480
aagacaggcc agcagcccgc taaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg atccacaacc tctcggagaa cctccagcaa ccccgctgc tgtgggacct 600
actacaatgg ctccaggcgg tggcgacca atggcagaca ataacgaagg cccgacgga 660
gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcca cagagtcac 720
accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780
tccagtgtct caacgggggc cagcaacgac aaccactact tcggctacag caccctctg 840
gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900
atcaacaaca attggggatt ccggcccaag agactcaact tcaaaactct caacatccaa 960
gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcac 1020
gttcaagtct tctcggactc ggagtaccag ctccgtacg tctcggctc tgcgcaccag 1080
ggctgcctcc ctccgttccc ggcggacgtg ttcattgatt cgcaatacgg ctacctgac 1140
ctcaacaatg gcagccaagc cgtgggacgt tcacctttt actgcctgga atatttccct 1200
tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260
ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

```

caatacctgt attacccgaa cagaactcaa aatcagtcg gaagtgccca aaacaaggac 1380
 ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
 ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500
 tttaacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560
 ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgc 1620
 atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680
 acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740
 gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800
 gcattacctg gcatgggtgt gcaaggtaga gacgtgtacc tgcagggtcc catttggggc 1860
 aaaattcctc acacagatgg acactttcac ccgtctctc ttatgggcgg ctttggactc 1920
 aagaaccgcg ctctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980
 gagttttcag ctacaaagt tgcctcattc atcaccaat actccacagg acaagtgagt 2040
 gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100
 tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
 tatactgagc ctgcgcccat tggcaccgt taccttacc gtcccctgta a 2211

<210> 82
 <211> 2211
 <212> DNA
 <213> new AAV serotype, clone hu.46

<400> 82
 atggctgccc acggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtga agctcaaac tggcccacca ccaccaaac ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgcc ttaagaaga tacgtctttt gggggcaacc tcgggcgggc agtcttccag 360
 gccaagaagc ggggtctcga acctctcggc ctggttgagg aaggcgctaa gacggctcct 420
 ggaaagaaac gtccggtaga gcagtcgcca caagagccag actccccctc gggcatcggc 480
 aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540
 tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600
 actacaatgg cttcaggcgg tggcgacce atggcagaca ataacgaagg cgccgacgga 660
 gtgggtaatg cctcaggaaa ttggcactgc gattccacat ggctgggcga cagagtcac 720
 accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780
 tccagtgtct caacgggggc cagcaacgac aaccactact tcggctacag caccctctgg 840
 ggggtatttt atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900
 atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960
 gtcaaggagg tcacgacgaa tgatggcgct acaaccatcg ctaataacct taccagcacg 1020
 gttcaagtct tctcgactc ggagtaccag ctccgtacg tcctcggtc tgcgcaccag 1080
 ggccgcctcc ctccgttccc ggcggacgtg ttcattgatt cgcaatacgg ctacctgacg 1140
 ctcaacaatg gcagccaagc cgtgggacgt tcatcctctt actgcctgga atatttccct 1200
 tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260
 ctccacagca gctgcgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320
 caatacctgt attacctgaa cagaactcaa aatcagtcg gaagtgccca aaacaggac 1380
 ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
 ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500
 tttaacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560
 ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgc 1620

```

atgatttttg gaaaagagag cgccggagct tcaaactg cattggacaa tgcatgatt 1680
acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740
gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800
gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcaggggcc catttgggcc 1860
aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920
aagaaccgcg ctctcagat cctcatcaaa aacacgcctg ttcttgcgaa tcctccggcg 1980
gagttttcag ctacaaagtt tgcttcattc atcacccaat actccgcagg acaagtgagt 2040
gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100
tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcacccgt taccttacct gtccttgta a 2211

```

```

<210> 83
<211> 738
<212> PRT
<213> vp1, clone hu.17
<400> 83

```

```

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```

```

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```

```

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```

```

Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```

```

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```

```

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```

```

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```

```

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```

```

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```

```

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

```

```

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

```

```

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

```

```

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

```

```

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

```

```

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

```

```

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

```

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile

610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 84
 <211> 738
 <212> PRT
 <213> vp1, clone hu.6

<400> 84

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly

195	200	205
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 210 215 220		
Ser Ser Gly Asn Trp His Cys Asp Ser Ala Trp Leu Gly Asp Arg Val 225 230 235 240		
Ile Thr Thr Ser Thr Arg Pro Trp Ala Leu Pro Thr Tyr Asn Asn His 245 250 255		
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp 260 265 270		
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn 275 280 285		
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn 290 295 300		
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn 305 310 315 320		
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala 325 330 335		
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln 340 345 350		
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe 355 360 365		
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn 370 375 380		
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr 385 390 395 400		
Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr 405 410 415		
Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser 420 425 430		
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu 435 440 445		
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu 450 455 460		
Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp 465 470 475 480		
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser 485 490 495		
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His 500 505 510		
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr 515 520 525		
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met 530 535 540		
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val 545 550 555 560		

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 85
<211> 738
<212> PRT
<213> vp1, clone hu.42

<400> 85

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Ser Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Leu
 625 630 635 640
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 86
 <211> 738
 <212> PRT
 <213> vp1, clone rh.38

<400> 86

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Arg Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Pro Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 87
 <211> 738
 <212> PRT
 <213> vp1, clone hu.40

<400> 87

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Ser Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Glu Phe Ser Tyr

405 410 415
 Thr Phe Glu Asp val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 88
 <211> 738
 <212> PRT
 <213> vp1, clone hu.37

<400> 88

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 89
<211> 738
<212> PRT
<213> vp1, clone rh.39

<400> 89

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 90
 <211> 738
 <212> PRT
 <213> vp1, clone AAV4407
 <400> 90

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile

610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 91
 <211> 738
 <212> PRT
 <213> vp1, clone hu.41

<400> 91

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Pro Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly

195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Val Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 92
 <211> 738
 <212> PRT
 <213> vp1, clone rh.40

<400> 92

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Gln Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asp Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Arg Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 93
 <211> 731
 <212> PRT
 <213> vp1, clone pi.1

<400> 93

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln
 145 150 155 160
 Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
 165 170 175
 Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
 180 185 190
 Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
 195 200 205
 Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His
 210 215 220
 Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
 225 230 235 240
 Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
 245 250 255
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
 260 265 270
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
 275 280 285
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
 290 295 300
 Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
 305 310 315 320
 Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
 325 330 335
 Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
 340 345 350
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
 355 360 365
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
 370 375 380
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
 385 390 395 400
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
 405 410 415
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
 420 425 430
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
 435 440 445
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
 450 455 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
 465 470 475 480
 Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
 485 490 495
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
 500 505 510
 Val Ser Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
 515 520 525
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
 530 535 540
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
 545 550 555 560
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
 565 570 575
 Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
 580 585 590
 Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
 595 600 605
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
 610 615 620
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
 625 630 635 640
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
 645 650 655
 Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
 660 665 670
 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
 675 680 685
 Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
 690 695 700
 Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
 705 710 715 720
 Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730

<210> 94
 <211> 731
 <212> PRT
 <213> vp1, clone pi.3

<400> 94

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val⁶⁵ Asn Glu Ala Asp⁷⁰ Ala Ala Ala Leu Glu⁷⁵ His Asp Lys Ala Tyr Asp⁸⁰
 Gln Gln Leu Lys⁸⁵ Gly Asp Asn Pro Tyr⁹⁰ Leu Arg Tyr Asn His⁹⁵ Ala
 Asp Ala Glu¹⁰⁰ Phe Gln Glu Arg Leu¹⁰⁵ Gln Glu Asp Thr Ser Phe¹¹⁰ Gly Gly
 Asn Leu¹¹⁵ Gly Arg Ala Val Phe¹²⁰ Gln Ala Lys Lys Arg Val¹²⁵ Leu Glu Pro
 Leu Gly¹³⁰ Leu Val Glu Glu¹³⁵ Gly Ala Lys Thr Ala Pro¹⁴⁰ Gly Lys Lys Arg
 Pro Val¹⁴⁵ Glu Pro Asp¹⁵⁰ Ser Ser Ser Gly Ile¹⁵⁵ Gly Lys Ser Gly Gln Gln¹⁶⁰
 Pro Ala Lys Lys¹⁶⁵ Arg Leu Asn Phe Gly¹⁷⁰ Pro Thr Gly Asp Ser Glu¹⁷⁵ Ser
 Val Pro Asp¹⁸⁰ Pro Gln Pro Leu Ser¹⁸⁵ Glu Pro Pro Ala Gly¹⁹⁰ Pro Ser Gly
 Leu Gly¹⁹⁵ Ser Gly Thr Met Ala²⁰⁰ Ala Gly Gly Gly Ala Pro²⁰⁵ Met Ala Asp
 Asn Asn²¹⁰ Glu Gly Ala Asp²¹⁵ Gly Val Gly Asn Val²²⁰ Ser Gly Asn Trp His
 Cys²²⁵ Asp Ser Thr Trp Leu²³⁰ Gly Asp Arg Val²³⁵ Ile Thr Thr Ser Thr Arg²⁴⁰
 Thr Trp Ala Leu²⁴⁵ Thr Tyr Asn Asn²⁵⁰ His Leu Tyr Lys Gln Ile²⁵⁵ Ser
 Asn Gly Thr²⁶⁰ Ser Gly Gly Ser Ser²⁶⁵ Asn Asp Asn Thr Tyr Phe²⁷⁰ Gly Tyr
 Ser Thr²⁷⁵ Pro Trp Gly Tyr Phe²⁸⁰ Asp Phe Asn Arg Phe²⁸⁵ His Cys His Phe
 Ser Pro²⁹⁰ Arg Asp Trp Gln Arg²⁹⁵ Leu Ile Asn Asn³⁰⁰ Asn Trp Gly Phe Arg
 Pro Lys Lys Leu Asn³¹⁰ Phe Lys Leu Phe Asn³¹⁵ Ile Gln Val Lys Glu Val³²⁰
 Thr Gln Asn Glu Gly³²⁵ Thr Lys Thr Thr Ala³³⁰ Asn Asn Leu Thr Ser³³⁵ Thr
 Val Gln Val³⁴⁰ Phe Thr Asp Ser Glu Tyr³⁴⁵ Gln Leu Pro Tyr Val³⁵⁰ Leu Gly
 Ser Ala His³⁵⁵ Gln Gly Cys Leu Pro³⁶⁰ Pro Phe Pro Ala Asp³⁶⁵ Val Phe Met
 Ile Pro³⁷⁰ Gln Tyr Gly Tyr Leu³⁷⁵ Thr Leu Asn Asn³⁸⁰ Gly Ser Gln Ala Val
 Gly Arg Ser Ser Phe Tyr³⁹⁰ Cys Leu Glu Tyr Phe³⁹⁵ Pro Ser Gln Met Leu⁴⁰⁰
 Arg Thr Gly Asn Asn⁴⁰⁵ Phe Thr Phe Ser Tyr⁴¹⁰ Thr Phe Glu Asp Val⁴¹⁵ Pro
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn

420 425 430
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
 435 440 445
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
 450 455 460
 Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
 465 470 475 480
 Gln Gln Arg Val Ser Thr Ala Val Ser Gln Asn Asn Ser Asn Phe
 485 490 495
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
 500 505 510
 Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
 515 520 525
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
 530 535 540
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
 545 550 555 560
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
 565 570 575
 Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
 580 585 590
 Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
 595 600 605
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
 610 615 620
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
 625 630 635 640
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
 645 650 655
 Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
 660 665 670
 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
 675 680 685
 Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
 690 695 700
 Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
 705 710 715 720
 Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730

<210> 95
 <211> 731
 <212> PRT
 <213> vp1, clone pi.2

<400> 95

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Arg Gln
 145 150 155 160
 Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
 165 170 175
 Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
 180 185 190
 Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
 195 200 205
 Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His
 210 215 220
 Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
 225 230 235 240
 Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
 245 250 255
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
 260 265 270
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
 275 280 285
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
 290 295 300
 Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
 305 310 315 320
 Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
 325 330 335
 Val Gln Val Phe Thr Asp Ser Lys Tyr Gln Leu Pro Tyr Val Leu Gly
 340 345 350
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
 355 360 365
 Ile pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
 370 375 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
 385 390 395 400
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
 405 410 415
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
 420 425 430
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
 435 440 445
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
 450 455 460
 Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
 465 470 475 480
 Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
 485 490 495
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
 500 505 510
 Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
 515 520 525
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
 530 535 540
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
 545 550 555 560
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
 565 570 575
 Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
 580 585 590
 Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
 595 600 605
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
 610 615 620
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
 625 630 635 640
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
 645 650 655
 Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
 660 665 670
 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
 675 680 685
 Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
 690 695 700
 Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
 705 710 715 720
 Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730

<210> 96
 <211> 738
 <212> PRT

<213> H₂O, 100°C, 1h, 52

<400> 96

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190
Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335
Asn Ser Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Ser Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 97
<211> 738
<212> PRT
<213> vp1, clone rh.53

<400> 97

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Val His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Ser Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe

660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg
 725 730 735
 Asn Leu

<210> 98
 <211> 738
 <212> PRT
 <213> vp1, clone rh.70

<400> 98

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Ala Tyr Asn Asn His

Page 107

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Ser
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 99
 <211> 738
 <212> PRT
 <213> vp1, clone rh.64
 <400> 99

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Arg Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 100
<211> 738
<212> PRT
<213> vp1, clone rh.68
<400> 100

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Pro Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Val Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Leu Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 101
 <211> 738
 <212> PRT
 <213> vp1, clone rh.46

<400> 101

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu

450 455 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 102
 <211> 738
 <212> PRT
 <213> vp1, clone hu.39

<400> 102

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Arg
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Leu Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Ala Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Pro Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400

<210>	103
<211>	738
<212>	PRT

<213> "vp1, clone rh.49"

<400> 103

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Arg Tyr Asn His Ala
85 90 95Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Leu Ile Gly Glu Pro
180 185 190Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Asn Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Met Gly Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Gly Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 104
 <211> 738
 <212> PRT
 <213> vp1, clone rh.51

<400> 104

Met Val Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Leu Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300

Asn 305 Asn Trp Gly Phe Arg 310 Pro Lys Arg Leu Ser 315 Phe Lys Leu Phe Asn 320
 Ile Gln Val Lys Glu 325 Val Thr Gln Asn Glu 330 Gly Thr Lys Thr Ile 335 Ala
 Asn Asn Leu Thr 340 Ser Thr Ile Gln Val 345 Phe Thr Asp Ser Glu 350 Tyr Gln
 Leu Pro Tyr 355 Val Leu Gly Ser Ala 360 His Gln Gly Cys Gln 365 Pro Pro Phe
 Pro Ala 370 Asp Val Phe Met Ile 375 Pro Gln Tyr Gly Tyr 380 Leu Thr Leu Asn
 Asn 385 Gly Ser Gln Ala Val 390 Gly Arg Ser Ser Phe 395 Tyr Cys Leu Glu Tyr 400
 Phe Pro Ser Gln Met 405 Leu Arg Thr Gly Asn 410 Asn Phe Ser Phe Ser 415 Tyr
 Thr Phe Glu Asp 420 Val Pro Phe His Ser 425 Ser Tyr Ala His Ser 430 Gln Ser
 Leu Asp Arg 435 Leu Met Asn Pro Leu 440 Ile Asp Gln Tyr Leu 445 Tyr Tyr Leu
 Ser Arg 450 Thr Gln Ser Thr Gly 455 Gly Thr Ala Gly Thr 460 Gln Gln Leu Leu
 Phe 465 Ser Gln Ala Gly Pro 470 Ser Asn Met Ser Ala 475 Gln Ala Arg Asn Trp 480
 Leu Pro Gly Pro Cys 485 Tyr Arg Gln Gln Arg 490 Val Ser Thr Thr Leu 495 Ser
 Gln Asn Asn Asn 500 Ser Asn Phe Ala Trp 505 Thr Gly Ala Thr Lys 510 Tyr His
 Leu Asn Gly 515 Arg Asp Ser Leu Val 520 Asn Pro Gly Val Ala 525 Met Ala Thr
 Asn Lys 530 Asp Asp Glu Asp Arg 535 Phe Phe Pro Ser Ser 540 Gly Ile Leu Met
 Phe 545 Gly Lys Gln Gly Ala 550 Gly Lys Asp Asn Val 555 Asp Tyr Ser Asn Val 560
 Met Leu Thr Ser Glu 565 Glu Glu Ile Lys Thr 570 Thr Asn Pro Val Ala 575 Thr
 Glu Gln Tyr Gly 580 Val Val Ala Asp Asn 585 Leu Gln Gln Gln Asn 590 Thr Ala
 Pro Ile Val 595 Gly Ala Val Asn Ser 600 Gln Gly Ala Leu Pro 605 Gly Met Val
 Trp Gln 610 Asn Arg Asp Val Tyr 615 Leu Gln Gly Pro Ile 620 Trp Ala Lys Ile
 Pro 625 His Thr Asp Gly Asn 630 Phe His Pro Ser Pro 635 Leu Met Gly Gly Phe 640
 Gly Leu Lys His Pro 645 Pro Pro Gln Ile Leu 650 Ile Lys Asn Thr Pro 655 Val
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe

"660"

665

670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Pro Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735
 Asn Leu

<210> 105
 <211> 738
 <212> PRT
 <213> vp1, clone rh.57

<400> 105

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His

245
 250 255
 Leu Tyr Lys Gln Thr Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Ala Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 106
 <211> 738
 <212> PRT
 <213> vp1, clone rh.58

<400> 106

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Cys Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 107
<211> 738
<212> PRT
<213> vp1, clone rh.61

<400> 107

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Pro Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Pro Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asp Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Val Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 108
 <211> 738
 <212> PRT
 <213> vp1, clone rh.50

<400> 108

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Gly Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu

450^{ind} 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Ser Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 109
 <211> 737
 <212> PRT
 <213> vpl, clone rh.45

<400> 109

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35

40

45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445
 Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe
 450 455 460
 Ser Gln Ala Gly Pro Ser Asn Met Ser Thr Gln Ala Arg Asn Trp Leu
 465 470 475 480
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln
 485 490 495
 Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
 500 505 510
 Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr Asn
 515 520 525
 Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met Phe
 530 535 540
 Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val Met
 545 550 555 560
 Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
 580 585 590
 Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
 705 710 715 720
 Ala Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735

Leu

<210> 110
 <211> 738
 <212> PRT

<213> "vp1," clone rh.59"

<400> 110

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Pro Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350

Pro Tyr Val₃₅₅ Leu Gly Ser Ala His₃₆₀ Gln Gly Cys Leu Pro₃₆₅ Pro Phe Pro
 Ala Asp Val₃₇₀ Phe Met Ile Pro₃₇₅ Gln Tyr Gly Tyr Leu₃₈₀ Thr Leu Asn Asn
 Gly Ser Gln Ser Val₃₉₀ Gly Arg Ser Ser Phe Tyr₃₉₅ Cys Leu Glu Tyr Phe₄₀₀
 Pro Ser Gln Met Leu₄₀₅ Arg Thr Gly Asn Asn₄₁₀ Phe Thr Phe Ser Tyr₄₁₅ Thr
 Phe Glu Asp Val₄₂₀ Pro Phe His Ser Ser₄₂₅ Tyr Ala His Ser Gln₄₃₀ Ser Leu
 Asp Arg Leu₄₃₅ Met Asn Pro Leu Ile₄₄₀ Asp Gln Tyr Leu Tyr₄₄₅ Tyr Leu Ala
 Arg Thr Gln Ser Asn Ala Gly₄₅₅ Gly Thr Ala Gly Asn₄₆₀ Arg Glu Leu Gln
 Phe Tyr Gln Gly Gly Pro₄₇₀ Thr Thr Met Ala Glu₄₇₅ Gln Ala Lys Asn Trp₄₈₀
 Leu Pro Gly Pro Cys₄₈₅ Tyr Arg Gln Gln Arg₄₉₀ Val Ser Thr Thr Leu Ser₄₉₅
 Gln Asn Asn Asn₅₀₀ Ser Asn Phe Ala Trp₅₀₅ Thr Gly Ala Thr Lys₅₁₀ Tyr His
 Leu Asn Gly₅₁₅ Arg Asp Ser Leu Val₅₂₀ Asn Pro Gly Val Ala₅₂₅ Met Ala Thr
 Asn Lys₅₃₀ Asp Asp Glu Asp Arg₅₃₅ Phe Phe Pro Ser Ser₅₄₀ Gly Ile Leu Met
 Phe Gly Lys Gln Gly Ala₅₅₀ Gly Lys Asp Asn Val₅₅₅ Asp Tyr Ser Asn Val₅₆₀
 Met Leu Thr Ser Glu₅₆₅ Glu Glu Ile Lys Thr₅₇₀ Thr Asn Pro Val Ala Thr₅₇₅
 Glu Gln Tyr Gly₅₈₀ Val Val Ala Asp Asn₅₈₅ Leu Gln Gln Gln Asn₅₉₀ Thr Ala
 Pro Ile Val₅₉₅ Gly Ala Val Asn Ser₆₀₀ Gln Gly Ala Leu Pro₆₀₅ Gly Met Val
 Trp Gln Asn Arg Asp Val Tyr₆₁₅ Leu Gln Gly Pro Ile₆₂₀ Trp Ala Lys Ile
 Pro His Thr Asp Gly Asn₆₃₀ Phe His Pro Ser Pro₆₃₅ Leu Met Gly Gly Phe₆₄₀
 Gly Leu Lys His Pro₆₄₅ Pro Pro Gln Ile Leu₆₅₀ Ile Lys Asn Thr Pro Val₆₅₅
 Pro Ala Asp Pro₆₆₀ Pro Thr Ala Phe Asn₆₆₅ Gln Ala Lys Leu Asn₆₇₀ Ser Phe
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile₆₈₅ Glu Trp Glu
 Leu Gln Lys Glu Asn Ser Lys₆₉₅ Arg Trp Asn Pro Glu₇₀₀ Ile Gln Tyr Thr
 Ser Asn Tyr Tyr Lys Ser₇₁₀ Thr Asn Val Asp Phe₇₁₅ Ala Val Asn Thr Glu₇₂₀

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 111
<211> 737
<212> PRT
<213> vp1, clone rh.44
<400> 111

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Cys Asp
65 70 75 80

Gln Arg Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
260 265 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile

660

665

670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Asp Glu Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735
 Leu

<210> 112
 <211> 737
 <212> PRT
 <213> vp1, clone rh.65

<400> 112

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His

245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Arg Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735
 Leu

<210> 113
 <211> 737
 <212> PRT
 <213> vp1, clone rh.67

<400> 113

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560

Met Thr Asn Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
565 570 575
Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
580 585 590
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640
Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655
Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685
Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700
Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720
Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 114
<211> 737
<212> PRT
<213> vp1, clone rh.62
<400> 114

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125
Leu Gly Leu Ala Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Gly Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Asp Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735

Leu

<210> 115
 <211> 737
 <212> PRT
 <213> vp1, clone rh.48

<400> 115

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln

450 455 460
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735
 Leu

<210> 116
 <211> 737
 <212> PRT
 <213> vp1, clone rh.54

<400> 116

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400

Pro Ser Gln Val Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ser Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735
 Leu

<210> 117
 <211> 737
 <212> PRT

<213> vpl, clone rh.55

<400> 117

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Arg Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 118
<211> 738
<212> PRT
<213> vp1, clone rh.47

<400> 118

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys His Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn 305 Asn Trp Gly Phe Arg 310 Pro Lys Arg Leu Ser 315 Phe Lys Leu Phe Asn 320
 Ile Gln Val Lys Glu 325 Val Thr Gln Asn Glu 330 Gly Thr Lys Thr Ile 335 Ala
 Asn 340 Asn Leu Thr 340 Ser Thr Val Gln Val 345 Phe Ser Asp Ser Glu 350 Tyr Gln
 Leu Pro Tyr 355 Val Leu Gly Ser Ala 360 His Gln Gly Cys Leu 365 Pro Pro Phe
 Pro Ala 370 Asp Val Phe Met Ile 375 Pro Gln Tyr Gly Tyr 380 Leu Thr Leu Asn
 Asn 385 Gly Ser Gln Ser Val 390 Gly Arg Ser Ser Phe 395 Tyr Cys Leu Glu Tyr 400
 Phe Pro Ser Gln Met 405 Leu Arg Thr Gly Asn 410 Asn Phe Thr Phe Ser 415 Tyr
 Thr Phe Glu Asp 420 Val Pro Phe His Ser 425 Ser Tyr Ala His Ser 430 Gln Ser
 Leu Asp Arg 435 Leu Met Asn Pro Leu 440 Ile Asp Gln Tyr Leu Tyr Tyr Leu
 Ala Arg 450 Thr Gln Ser Asn Ala 455 Gly Gly Thr Ala Gly 460 Asn Arg Glu Leu
 Gln 465 Phe Tyr Gln Gly Gly 470 Pro Thr Thr Met Ala 475 Glu Gln Ala Lys Asn 480
 Trp Leu Pro Gly Pro 485 Cys Phe Arg Gln Gln 490 Arg Val Ser Lys Thr 495 Leu
 Asp Gln Asn Asn 500 Asn Ser Asn Phe Ala 505 Trp Thr Gly Ala Thr 510 Lys Tyr
 His Leu 515 Asn Gly Arg Asn Ser Leu 520 Val Asn Pro Gly Val 525 Ala Met Ala
 Thr His 530 Lys Asp Asp Glu Glu 535 Arg Phe Phe Pro Ser 540 Ser Gly Val Leu
 Ile 545 Phe Gly Lys Thr Gly 550 Ala Ala Asn Lys Thr 555 Thr Leu Glu Asn Val 560
 Leu Met Thr Asn Glu 565 Glu Glu Ile Arg Pro 570 Thr Asn Pro Val Ala Thr 575
 Glu Glu Tyr Gly 580 Thr Val Ser Ser Asn 585 Leu Gln Ala Ala Asn 590 Thr Ala
 Ala Gln Thr 595 Gln Val Val Asn Asn 600 Gln Gly Ala Leu Pro 605 Gly Met Val
 Trp Gln 610 Asn Arg Asp Val Tyr 615 Leu Gln Gly Pro Ile 620 Trp Ala Lys Ile
 Pro 625 His Thr Asp Gly Asn 630 Phe His Pro Ser Pro 635 Leu Met Gly Gly Phe 640
 Gly Leu Lys His Pro 645 Pro Pro Gln Ile Leu 650 Ile Lys Asn Thr Pro 655 Val
 Pro Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe

660

665

670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 119
 <211> 737
 <212> PRT
 <213> vp1, clone rh.69

<400> 119

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His

Page 152

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735

Leu

<210> 120
 <211> 735
 <212> PRT
 <213> vp1, clone rh.60

<400> 120

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile His Glu Trp Trp Asp Pro Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr His Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Glu Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560

Met Thr Asn Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
565 570 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Phe
690 695 700

Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 121
<211> 736
<212> PRT
<213> vp1, clone hu.31

<400> 121

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
 370 375 380
 Gly Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
 405 410 415
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445
 Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
 450 455 460
 Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
 465 470 475 480
 Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
 485 490 495
 Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
 500 505 510
 Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
 515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
 530 535 540
 Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
 545 550 555 560
 Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
 565 570 575
 Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
 580 585 590
 Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val
 705 710 715 720
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 122
 <211> 736
 <212> PRT
 <213> vp1, clone hu.32
 <400> 122
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
 145 150 155 160
 Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
 370 375 380
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
 405 410 415
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445
 Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
 450 455 460
 Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
 465 470 475 480
 Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn

485 490 495
 Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
 500 505 510
 Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
 515 520 525
 Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
 530 535 540
 Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
 545 550 555 560
 Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
 565 570 575
 Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
 580 585 590
 Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
 705 710 715 720
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 123
 <211> 736
 <212> PRT
 <213> capsid of hu.14\AAV9

<400> 123

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
 145 150 155 160
 Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
 370 375 380
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
 405 410 415
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 124

<211> 735

<212> PRT

<213> vp1, clone hu.33

<400> 124

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Gly Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 125
 <211> 735
 <212> PRT
 <213> vp1, clone hu.34
 <400> 125
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Glu Ser
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 126

<211> 735
 <212> PRT
 <213> vp1, clone hu.36

<400> 126

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr

340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Ala Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 127
 <211> 735
 <212> PRT
 <213> vp1, clone hu.45
 <400> 127
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Pro Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Val Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 128
 <211> 735
 <212> PRT
 <213> vp1, clone hu.47
 <400> 128
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Ser His Tyr
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 129
 <211> 735
 <212> PRT
 <213> vpl, clone hu.13

<400> 129

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Gly Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp

595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 130
 <211> 735
 <212> PRT
 <213> vp1, clone hu.28
 <400> 130

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Ser Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly

195	200	205
Ala Pro Met Ala Asp Asn 210	Asn Glu Gly Ala Asp Gly 215	Val Gly Asn Ser 220
Ser Gly Asn Trp His 225	Cys Asp Ser Thr Trp 230	Met Gly Asp Arg Val Ile 235
Thr Thr Ser Thr Arg 245	Thr Trp Ala Leu Pro 250	Thr Tyr Asn Asn His Leu 255
Tyr Lys Gln Ile Ser Ser Gln Ser 260	Gly Ala Ser Asn Asp Asn His Tyr 265	
Phe Gly Tyr Ser Thr Pro Trp 275	Gly Tyr Phe Asp Phe Asn Arg Phe His 280	
Cys His Phe Ser Pro Arg 290	Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp 295	
Gly Phe Arg Pro Lys Arg 305	Leu Asn Phe Lys Leu Phe Asn Ile Gln Val 310	
Lys Glu Val Thr Gln 325	Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu 330	
Thr Ser Thr Val Gln Val Phe Thr 340	Asp Ser Glu Tyr Gln Leu Pro Tyr 345	
Val Leu Gly Ser Ala His Gln 355	Gly Cys Leu Pro Pro Phe Pro Ala Asp 360	
Val Phe Met Val Pro Gln Tyr 370	Gly Tyr Leu Thr Leu Asn Asn Gly Ser 375	
Gln Ala Val Gly Arg Ser 385	Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser 390	
Gln Met Leu Arg Thr 405	Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu 410	
Asp Val Pro Phe His Ser Ser Tyr 420	Ala His Ser Gln Ser Leu Asp Arg 425	
Leu Met Asn Pro Leu Ile Asp 435	Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr 440	
Asn Thr Pro Ser Gly Thr Thr Thr 450	Gln Ser Arg Leu Gln Phe Ser Gln 455	
Ala Gly Ala Ser Asp Ile Gln Asp Gln Ser 465	Arg Asn Trp Leu Pro Gly 470	
Pro Cys Tyr Arg Gln Gln Arg Val Ser 485	Lys Thr Ser Ala Asp Asn Asn 490	
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His 500	Leu Asn Gly 505	
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp 515		
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys 530		
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr 545		

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Gly Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Thr Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 131
 <211> 735
 <212> PRT
 <213> vp1, clone hu.30
 <400> 131
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

165 170 175
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Ser Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 132
 <211> 735
 <212> PRT
 <213> vp1, clone hu.29
 <400> 132
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Gly Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

 <210> 133
 <211> 735
 <212> PRT
 <213> vp1, clone hu.19

 <400> 133
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Glu Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp Tyr Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln

450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 134
 <211> 735
 <212> PRT
 <213> vp1, clone hu.20

<400> 134

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Val
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Ala Ala Pro Gly Glu Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly His Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Pro Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Ala Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 135
 <211> 735
 <212> PRT
 <213> vp1, clone hu.21
 <400> 135
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 136
 <211> 735

<212> PRT
 <213> vp1, clone hu.24
 <400> 136
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr

705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

 <210> 137
 <211> 735
 <212> PRT
 <213> vp1, clone hu.23-2

 <400> 137
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125

 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205

 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Cys Asn Asn His Leu
 245 250 255

 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285

 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val

305	310	315	320
Lys Glu Val Thr	Gln Asn Asp Gly Thr	Thr Thr Ile Ala Asn	Asn Leu
	325	330	335
Thr Ser Thr	Val Gln Val Phe Thr	Asp Ser Glu Tyr Gln	Leu Pro Tyr
	340	345	350
Val Leu Gly	Ser Ala His Gln Gly	Cys Leu Pro Pro	Phe Pro Ala Asp
	355	360	365
Val Phe Met Val	Pro Gln Tyr Gly Tyr	Leu Thr Leu Asn Asn	Gly Ser
	370	375	380
Gln Ala Val Gly	Arg Ser Ser Phe Tyr Cys	Leu Glu Tyr Phe Pro	Ser
	385	390	400
Gln Met Leu Arg	Thr Gly Asn Asn Phe	Thr Phe Ser Tyr Thr	Phe Glu
	405	410	415
Asp Val Pro	Phe His Ser Ser Tyr	Ala His Ser Gln Ser	Leu Asp Arg
	420	425	430
Leu Met Asn	Pro Leu Ile Asp Gln	Tyr Leu Tyr Tyr	Leu Ser Arg Thr
	435	440	445
Asn Thr Pro	Ser Gly Thr Thr	Thr Met Ser Arg	Leu Gln Phe Ser Gln
	450	455	460
Ala Gly Ala Ser	Asp Ile Arg Asp Gln Ser	Arg Asn Trp Leu Pro	Gly
	465	470	475
Pro Cys Tyr Arg	Gln Gln Arg Val Ser	Lys Thr Ala Ala Asp	Asn Asn
	485	490	495
Asn Ser Asp	Tyr Ser Trp Thr Gly	Ala Thr Lys Tyr His	Leu Asn Gly
	500	505	510
Arg Asp Ser	Leu Val Asn Pro Gly	Pro Ala Met Ala Ser	His Lys Asp
	515	520	525
Asp Glu Glu	Lys Tyr Phe Pro Gln Ser Gly	Val Leu Ile Phe Gly	Lys
	530	535	540
Gln Asp Ser Gly	Lys Thr Asn Val Asp Ile	Glu Lys Val Met Ile	Thr
	545	550	555
Asp Glu Glu Glu	Ile Arg Thr Thr	Asn Pro Val Ala Thr	Glu Gln Tyr
	565	570	575
Gly Ser Val	Ser Thr Tyr Leu Gln Ser	Gly Asn Thr Gln	Ala Ala Thr
	580	585	590
Ser Asp Val	Asn Thr Gln Gly Val	Leu Pro Gly Met Val	Trp Gln Asp
	595	600	605
Arg Asp Val	Tyr Leu Arg Gly	Pro Ile Trp Ala Lys	Ile Pro His Thr
	610	615	620
Asp Gly His Phe	His Pro Ser Pro Leu Met	Gly Gly Phe Gly Leu	Lys
	625	630	635
His Pro Pro Pro	Gln Ile Leu Ile Lys	Asn Thr Pro Val Pro	Ala Asn
	645	650	655
Pro Ser Thr	Thr Phe Ser Ala Ala	Lys Phe Ala Ser Phe	Ile Thr Gln
	660	665	670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 138
 <211> 735
 <212> PRT
 <213> vp1, clone hu.22

<400> 138

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Gly Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Gly Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Thr Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 139
 <211> 735
 <212> PRT
 <213> vp1, clone hu.26

<400> 139

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 140
 <211> 735
 <212> PRT
 <213> vp1, clone hu.27

<400> 140

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Gly Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Val Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Val Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Ala Ala Thr Glu Gln Tyr

565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Val Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

 <210> 141
 <211> 735
 <212> PRT
 <213> vp1, clone hu.4

 <400> 141
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

Page 198

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 142
 <211> 735
 <212> PRT
 <213> vp1, clone hu.5
 <400> 142
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly 130 Leu Val Glu Glu Pro 135 Val Lys Thr Ala Pro 140 Gly Lys Lys Arg
 Pro 145 Val Glu His Ser Pro 150 Val Glu Pro Asp Ser 155 Ser Ser Gly Thr Gly 160
 Lys Ala Gly Gln Gln Pro 165 Ala Arg Lys Arg 170 Leu Asn Phe Gly Gln Thr 175
 Gly Asp Ala Asp 180 Ser Val Pro Asp Pro 185 Gln Pro Leu Gly Gln Pro Pro 190
 Ala Ala Pro 195 Ser Gly Leu Gly Ser 200 Thr Thr Met Ala Thr 205 Gly Ser Gly
 Ala Pro 210 Met Ala Asp Asn Asn 215 Glu Gly Ala Asp Gly 220 Val Gly Asn Ser
 Ser 225 Gly Asn Trp His Cys 230 Asp Ser Gln Trp Leu 235 Gly Asp Arg Val Ile 240
 Thr Thr Ser Thr Arg 245 Thr Trp Ala Leu Pro 250 Thr Tyr Asn Asn His 255 Leu
 Tyr Lys Gln Ile 260 Ser Ser Gln Ser Gly 265 Ala Ser Asn Asp Asn 270 His Tyr
 Phe Gly Tyr 275 Ser Thr Pro Trp Gly 280 Tyr Phe Asp Phe Asn 285 Arg Phe His
 Cys His 290 Phe Ser Pro Arg Asp 295 Trp Gln Arg Leu Ile 300 Asn Asn Asn Trp
 Gly 305 Phe Arg Pro Lys Arg 310 Leu Asn Phe Lys Leu 315 Phe Asn Ile Gln Val 320
 Lys Glu Val Thr Gln 325 Asn Asp Gly Thr Thr 330 Thr Ile Ala Asn Asn 335 Leu
 Thr Ser Thr Val 340 Gln Val Phe Thr Asp 345 Ser Glu Tyr Gln Leu 350 Pro Tyr
 Val Leu Gly 355 Ser Ala His Gln Gly 360 Cys Leu Pro Pro Phe 365 Pro Ala Asp
 Val Phe 370 Met Val Pro Gln Tyr 375 Gly Tyr Leu Thr Leu 380 Asn Asn Gly Ser
 Gln 385 Ala Val Gly Arg Ser 390 Ser Phe Tyr Cys Leu 395 Glu Tyr Phe Pro Ser 400
 Gln Met Leu Arg Thr 405 Gly Asn Asn Phe Gln 410 Phe Ser Tyr Thr Phe 415 Glu
 Asp Val Pro Phe 420 His Ser Ser Tyr Ala 425 His Ser Gln Ser Leu 430 Asp Arg
 Leu Met Asn 435 Pro Leu Ile Asp Gln 440 Tyr Leu Tyr Tyr Leu 445 Asn Lys Thr
 Gln Thr 450 Asn Ser Gly Thr Leu 455 Gln Gln Ser Arg Leu 460 Leu Phe Ser Gln
 Ala Gly 465 Pro Thr Asn Met 470 Ser Leu Gln Ala Lys 475 Asn Trp Leu Pro Gly 480
 Pro Cys Tyr Arg Gln 485 Gln Arg Leu Ser Lys 490 Gln Ala Asn Asp Asn 495 Asn

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser Arg Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 143
 <211> 735
 <212> PRT
 <213> vp1, clone hu.2

<400> 143

Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Arg Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn Arg Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 144
 <211> 735
 <212> PRT
 <213> vp1, clone hu.1

<400> 144

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Gly Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg

420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Gly Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Thr Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 145
 <211> 736
 <212> PRT
 <213> vp1, clone hu.3

<400> 145

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro

20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Arg Pro Gly Leu Arg Lys Pro Val Lys Thr Ala Pro Gly Lys Lys
 130 135 140
 Arg Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr
 145 150 155 160
 Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro
 180 185 190
 Pro Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Asp Asp Arg Val
 225 230 235 240
 Ile Ala Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Cys Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
 405 410 415
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Cys Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys
 435 440 445
 Thr Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser
 450 455 460
 Gln Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn
 485 490 495
 Asn Asn Cys Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn
 500 505 510
 Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
 515 520 525
 Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly
 530 535 540
 Lys Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Gln
 565 570 575
 Tyr Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr
 580 585 590
 Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Met Ile Lys Ser Thr Pro Val Pro Ala
 645 650 655
 Asn Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Ser Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
 705 710 715 720
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 146
 <211> 735
 <212> PRT

2133 vpi; clone hu.25

<400> 146

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Gly Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asn Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 val Phe Met val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala val Gly Arg Ser Pro Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Thr val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr val Asn His Gln Gly Ala Leu Pro Gly Met val Trp Gln Asp
 595 600 605
 Arg Asp val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln val Ser val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser val Asn val Asp Phe Thr val Asp Asn Asn Gly val Tyr
 705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 147
 <211> 735
 <212> PRT
 <213> vp1, clone hu.15

<400> 147

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
 50 55 60

Val Asp Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285

Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Leu Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys

675

680

685

Glu Asp Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Pro Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 148
<211> 735
<212> PRT
<213> vp1, clone hu.16
<400> 148

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His

275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Tyr Val Ser Asn Asn Leu Gln Asp Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 149
 <211> 735
 <212> PRT
 <213> vp1, clone hu.18

<400> 149

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Glu Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Ser Gly Ser Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Leu Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ser Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg Asn Leu
 725 730 735
 <210> 150
 <211> 735
 <212> PRT
 <213> vp1, clone hu.7
 <400> 150
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Gly Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 151
 <211> 735
 <212> PRT
 <213> vp1, clone hu.8
 <400> 151
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Thr Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys

530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

 <210> 152
 <211> 735
 <212> PRT
 <213> vp1, clone rh.56

 <400> 152
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg

130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Gln Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Ser Asn Ser Gly Ala Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Arg Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 153
 <211> 735
 <212> PRT
 <213> vp1, clone hu.11
 <400> 153
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp¹⁰⁰ Ala¹⁰¹ Glu¹⁰² Phe¹⁰³ Gln¹⁰⁴ Glu¹⁰⁵ Arg¹⁰⁶ Leu¹⁰⁷ Lys¹⁰⁸ Glu¹⁰⁹ Asp¹¹⁰ Thr¹¹¹ Ser¹¹² Phe¹¹³ Gly¹¹⁴ Gly¹¹⁵
 Asn¹¹⁶ Leu¹¹⁷ Gly¹¹⁸ Arg¹¹⁹ Ala¹²⁰ Val¹²¹ Phe¹²² Gln¹²³ Ala¹²⁴ Lys¹²⁵ Lys¹²⁶ Arg¹²⁷ Val¹²⁸ Leu¹²⁹ Glu¹³⁰ Pro¹³¹
 Leu¹³² Gly¹³³ Leu¹³⁴ Val¹³⁵ Glu¹³⁶ Glu¹³⁷ Pro¹³⁸ Val¹³⁹ Lys¹⁴⁰ Thr¹⁴¹ Ala¹⁴² Pro¹⁴³ Gly¹⁴⁴ Lys¹⁴⁵ Lys¹⁴⁶ Arg¹⁴⁷
 Pro¹⁴⁸ Val¹⁴⁹ Glu¹⁵⁰ His¹⁵¹ Ser¹⁵² Pro¹⁵³ Val¹⁵⁴ Glu¹⁵⁵ Pro¹⁵⁶ Asp¹⁵⁷ Ser¹⁵⁸ Ser¹⁵⁹ Ser¹⁶⁰ Gly¹⁶¹ Thr¹⁶² Gly¹⁶³
 Lys¹⁶⁴ Ala¹⁶⁵ Gly¹⁶⁶ His¹⁶⁷ Gln¹⁶⁸ Pro¹⁶⁹ Ala¹⁷⁰ Arg¹⁷¹ Lys¹⁷² Arg¹⁷³ Leu¹⁷⁴ Asn¹⁷⁵ Phe¹⁷⁶ Gly¹⁷⁷ Gln¹⁷⁸ Thr¹⁷⁹
 Gly¹⁸⁰ Asp¹⁸¹ Ala¹⁸² Asp¹⁸³ Ser¹⁸⁴ Val¹⁸⁵ Pro¹⁸⁶ Asp¹⁸⁷ Pro¹⁸⁸ Gln¹⁸⁹ Pro¹⁹⁰ Leu¹⁹¹ Gly¹⁹² Gln¹⁹³ Pro¹⁹⁴ Pro¹⁹⁵
 Ala¹⁹⁶ Ala¹⁹⁷ Pro¹⁹⁸ Thr¹⁹⁹ Ser²⁰⁰ Leu²⁰¹ Gly²⁰² Ser²⁰³ Thr²⁰⁴ Thr²⁰⁵ Met²⁰⁶ Ala²⁰⁷ Thr²⁰⁸ Gly²⁰⁹ Ser²¹⁰ Gly²¹¹
 Ala²¹² Pro²¹³ Met²¹⁴ Ala²¹⁵ Asp²¹⁶ Asn²¹⁷ Asn²¹⁸ Glu²¹⁹ Gly²²⁰ Ala²²¹ Asp²²² Gly²²³ Val²²⁴ Gly²²⁵ Asn²²⁶ Ser²²⁷
 Ser²²⁸ Gly²²⁹ Asn²³⁰ Trp²³¹ His²³² Cys²³³ Asp²³⁴ Ser²³⁵ Gln²³⁶ Trp²³⁷ Leu²³⁸ Gly²³⁹ Asp²⁴⁰ Arg²⁴¹ Val²⁴² Ile²⁴³
 Thr²⁴⁴ Thr²⁴⁵ Ser²⁴⁶ Thr²⁴⁷ Arg²⁴⁸ Thr²⁴⁹ Trp²⁵⁰ Ala²⁵¹ Leu²⁵² Pro²⁵³ Thr²⁵⁴ Tyr²⁵⁵ Asn²⁵⁶ Asn²⁵⁷ His²⁵⁸ Leu²⁵⁹
 Tyr²⁶⁰ Lys²⁶¹ Gln²⁶² Ile²⁶³ Ser²⁶⁴ Ser²⁶⁵ Gln²⁶⁶ Ser²⁶⁷ Gly²⁶⁸ Ala²⁶⁹ Ser²⁷⁰ Asn²⁷¹ Asp²⁷² Asn²⁷³ His²⁷⁴ Tyr²⁷⁵
 Phe²⁷⁶ Gly²⁷⁷ Tyr²⁷⁸ Ser²⁷⁹ Thr²⁸⁰ Pro²⁸¹ Trp²⁸² Gly²⁸³ Tyr²⁸⁴ Phe²⁸⁵ Asp²⁸⁶ Phe²⁸⁷ Asn²⁸⁸ Arg²⁸⁹ Phe²⁹⁰ His²⁹¹
 Cys²⁹² His²⁹³ Phe²⁹⁴ Ser²⁹⁵ Pro²⁹⁶ Arg²⁹⁷ Asp²⁹⁸ Trp²⁹⁹ Gln³⁰⁰ Arg³⁰¹ Leu³⁰² Ile³⁰³ Asn³⁰⁴ Asn³⁰⁵ Asn³⁰⁶ Trp³⁰⁷
 Gly³⁰⁸ Phe³⁰⁹ Arg³¹⁰ Pro³¹¹ Lys³¹² Arg³¹³ Leu³¹⁴ Asn³¹⁵ Phe³¹⁶ Lys³¹⁷ Leu³¹⁸ Phe³¹⁹ Asn³²⁰ Ile³²¹ Gln³²² Val³²³
 Lys³²⁴ Glu³²⁵ Val³²⁶ Thr³²⁷ Gln³²⁸ Asn³²⁹ Asp³³⁰ Gly³³¹ Thr³³² Thr³³³ Thr³³⁴ Ile³³⁵ Ala³³⁶ Asn³³⁷ Asn³³⁸ Leu³³⁹
 Thr³⁴⁰ Ser³⁴¹ Thr³⁴² Val³⁴³ Gln³⁴⁴ Val³⁴⁵ Phe³⁴⁶ Thr³⁴⁷ Asp³⁴⁸ Ser³⁴⁹ Glu³⁵⁰ Tyr³⁵¹ Gln³⁵² Leu³⁵³ Pro³⁵⁴ Tyr³⁵⁵
 Val³⁵⁶ Leu³⁵⁷ Gly³⁵⁸ Ser³⁵⁹ Ala³⁶⁰ His³⁶¹ Gln³⁶² Gly³⁶³ Cys³⁶⁴ Leu³⁶⁵ Pro³⁶⁶ Pro³⁶⁷ Phe³⁶⁸ Pro³⁶⁹ Ala³⁷⁰ Asp³⁷¹
 Val³⁷² Phe³⁷³ Met³⁷⁴ Val³⁷⁵ Pro³⁷⁶ Gln³⁷⁷ Tyr³⁷⁸ Gly³⁷⁹ Tyr³⁸⁰ Leu³⁸¹ Thr³⁸² Leu³⁸³ Asn³⁸⁴ Asn³⁸⁵ Gly³⁸⁶ Ser³⁸⁷
 Gln³⁸⁸ Ala³⁸⁹ Val³⁹⁰ Gly³⁹¹ Arg³⁹² Ser³⁹³ Ser³⁹⁴ Phe³⁹⁵ Tyr³⁹⁶ Cys³⁹⁷ Leu³⁹⁸ Glu³⁹⁹ Tyr⁴⁰⁰ Phe⁴⁰¹ Pro⁴⁰² Ser⁴⁰³
 Gln⁴⁰⁴ Met⁴⁰⁵ Leu⁴⁰⁶ Arg⁴⁰⁷ Thr⁴⁰⁸ Gly⁴⁰⁹ Asn⁴¹⁰ Asn⁴¹¹ Phe⁴¹² Thr⁴¹³ Phe⁴¹⁴ Ser⁴¹⁵ Tyr⁴¹⁶ Thr⁴¹⁷ Phe⁴¹⁸ Glu⁴¹⁹
 Asp⁴²⁰ Val⁴²¹ Pro⁴²² Phe⁴²³ His⁴²⁴ Ser⁴²⁵ Ser⁴²⁶ Tyr⁴²⁷ Ala⁴²⁸ His⁴²⁹ Ser⁴³⁰ Gln⁴³¹ Ser⁴³² Leu⁴³³ Asp⁴³⁴ Arg⁴³⁵
 Leu⁴³⁶ Met⁴³⁷ Asn⁴³⁸ Pro⁴³⁹ Leu⁴⁴⁰ Ile⁴⁴¹ Asp⁴⁴² Gln⁴⁴³ Tyr⁴⁴⁴ Leu⁴⁴⁵ Tyr⁴⁴⁶ Tyr⁴⁴⁷ Leu⁴⁴⁸ Asn⁴⁴⁹ Arg⁴⁵⁰ Thr⁴⁵¹
 Gln⁴⁵² Ser⁴⁵³ Asn⁴⁵⁴ Ser⁴⁵⁵ Gly⁴⁵⁶ Thr⁴⁵⁷ Leu⁴⁵⁸ Gln⁴⁵⁹ Gln⁴⁶⁰ Ser⁴⁶¹ Arg⁴⁶² Leu⁴⁶³ Leu⁴⁶⁴ Phe⁴⁶⁵ Ser⁴⁶⁶ Gln⁴⁶⁷

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr Arg Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 154
 <211> 735
 <212> PRT
 <213> vp1, clone hu.12
 <400> 154
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Pro Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

 <210> 155
 <211> 735
 <212> PRT
 <213> vp1, clone hu.9

 <400> 155
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Gln Asp Asn Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Ser Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Cys Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Pro Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser

385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Cys Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 156
 <211> 735
 <212> PRT
 <213> vp1, clone hu.10

<400> 156

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Leu Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Gly Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360

Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Leu Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
450 455 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
485 490 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
580 585 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Tyr Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Arg Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 157
 <211> 736
 <212> PRT
 <213> vp1, clone hu.48
 <400> 157
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320

Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
 515 520 525
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540
 Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
 705 710 715 720
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735
 <210> 158
 <211> 736
 <212> PRT
 <213> vp1, clone hu.44
 <400> 158
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Glu Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala

Page 235

245 250 255
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr val Leu Gly Ser Ala His Gln Gly Arg Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380
 Ser Gln Ala Val Gly Arg Ser Ser Ser Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser
 450 455 460
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575
 Phe Gly Thr Val Ala val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys Asn Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Ala Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
 705 710 715 720
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735

<210> 160
 <211> 737
 <212> PRT
 <213> vp1, clone hu.43

<400> 160

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Pro Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
 260 265 270
 His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Val Gln Tyr Leu Tyr Tyr Leu Asn
 435 440 445
 Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
 450 455 460
 Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
 465 470 475 480
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
 485 490 495
 Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
 500 505 510
 Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
 515 520 525
 Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
 530 535 540
 Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
 545 550 555 560
 Ile Thr Asp Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
 565 570 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
 580 585 590
 Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
 690 695 700
 Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
 705 710 715 720
 Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
 725 730 735

Leu

<210> 161
 <211> 738
 <212> PRT
 <213> vp1, clone hu.38

<400> 161

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Cys His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 162
 <211> 736
 <212> PRT
 <213> vp1, clone rh.71

<400> 162

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro

465 " 470 475 480
 Gly Pro Cys Tyr Arg 485 Gln Gln Arg Val Ser 490 Lys Thr Lys Thr Asp 495 Asn
 Asn Asn Ser Asn 500 Phe Thr Trp Thr Gly 505 Ala Ser Lys Tyr Asn 510 Leu Asn
 Gly Arg Glu 515 Ser Ile Ile Asn Pro 520 Gly Thr Ala Met Ala 525 Ser His Lys
 Asp Asp 530 Glu Asp Lys Phe Phe 535 Pro Met Ser Gly Val 540 Met Ile Phe Gly
 Lys 545 Glu Ser Ala Gly Ala 550 Ser Asn Thr Ala Leu 555 Asp Asn Val Met Ile 560
 Thr Asp Glu Glu Glu 565 Ile Lys Ala Thr Asn 570 Pro Val Ala Thr Glu 575 Arg
 Phe Gly Thr Val 580 Ala Val Asn Phe Gln 585 Ser Ser Ser Thr Asp 590 Pro Ala
 Thr Gly Asp 595 Val His Ala Met Gly 600 Ala Leu Pro Gly Met 605 Val Trp Gln
 Asp Arg 610 Asp Val Tyr Leu Gln 615 Gly Pro Ile Trp Ala 620 Lys Ile Pro His
 Thr Asp Gly His Phe 630 His Pro Ser Pro Leu Met 635 Gly Gly Phe Gly Leu 640
 Lys Asn Pro Pro Pro 645 Gln Ile Leu Ile Lys 650 Asn Thr Pro Val Pro Ala 655
 Asn Pro Pro Ala 660 Glu Phe Ser Ala Thr 665 Lys Phe Ala Ser Phe 670 Ile Thr
 Gln Tyr Ser 675 Thr Gly Gln Val Ser 680 Val Glu Ile Glu Trp 685 Glu Leu Gln
 Lys Glu 690 Asn Ser Lys Arg Trp 695 Asn Pro Glu Val Gln 700 Tyr Thr Ser Asn
 Tyr Ala Lys Ser Ala Asn 710 Val Asp Phe Thr Val 715 Asp Asn Asn Gly Leu 720
 Tyr Thr Glu Pro Arg 725 Pro Ile Gly Thr Arg 730 Tyr Leu Thr Arg Pro 735 Leu

<210> 163
 <211> 736
 <212> PRT
 <213> vp1, clone rh.43

<400> 163

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

65	70	75	80
Gln Gln Leu Glu	Ala ₈₅ Gly Asp Asn Pro	Tyr ₉₀ Leu Arg Tyr Asn	His ₉₅ Ala
Asp Ala Glu Phe	Gln ₁₀₀ Glu Arg Leu	Gln ₁₀₅ Glu Asp Thr Ser	Phe ₁₁₀ Gly Gly
Asn Leu Gly	Arg ₁₁₅ Ala Val Phe	Gln ₁₂₀ Ala Lys Lys Arg	Val ₁₂₅ Leu Glu Pro
Leu Gly ₁₃₀ Leu Val	Glu Glu Gly ₁₃₅ Ala Lys Thr	Ala ₁₄₀ Pro Gly Lys Lys Arg	
Pro ₁₄₅ Val Glu Gln Ser	Pro ₁₅₀ Gln Glu Pro Asp	Ser ₁₅₅ Ser Ser Gly Ile	Gly ₁₆₀
Lys Lys Gly Gln	Gln ₁₆₅ Pro Ala Arg Lys	Arg ₁₇₀ Leu Asn Phe Gly	Gln ₁₇₅ Thr
Gly Asp Ser	Glu ₁₈₀ Ser Val Pro Asp	Pro ₁₈₅ Gln Pro Leu Gly	Glu ₁₉₀ Pro Pro
Ala Ala Pro	Ser ₁₉₅ Gly Val Gly	Pro ₂₀₀ Asn Thr Met Ala	Ala ₂₀₅ Gly Gly Gly
Ala Pro ₂₁₀ Met Ala Asp	Asn ₂₁₅ Asn Glu Gly Ala Asp	Gly ₂₂₀ Val Gly Ser Ser	
Ser ₂₂₅ Gly Asn Trp His	Cys ₂₃₀ Asp Ser Thr Trp	Leu ₂₃₅ Gly Asp Arg Val	Ile ₂₄₀
Thr Thr Ser Thr	Arg ₂₄₅ Thr Trp Ala Leu	Pro ₂₅₀ Thr Tyr Asn Asn	His ₂₅₅ Leu
Tyr Lys Gln	Ile ₂₆₀ Ser Asn Gly Thr	Ser ₂₆₅ Gly Gly Ala Thr	Asn ₂₇₀ Asp Asn
Thr Tyr Phe	Gly ₂₇₅ Tyr Ser Thr Pro	Trp ₂₈₀ Gly Tyr Phe Asp	Phe ₂₈₅ Asn Arg
Phe ₂₉₀ His Cys His Phe Ser	Pro ₂₉₅ Arg Asp Trp Gln	Arg ₃₀₀ Leu Ile Asn Asn	
Asn Trp Gly Phe Arg	Pro ₃₁₀ Lys Arg Leu Ser	Phe ₃₁₅ Lys Leu Phe Asn	Ile ₃₂₀
Gln Val Lys Glu	Val ₃₂₅ Thr Gln Asn Glu	Gly ₃₃₀ Thr Lys Thr Ile	Ala ₃₃₅ Asn
Asn Leu Thr	Ser ₃₄₀ Thr Ile Gln Val	Phe ₃₄₅ Thr Asp Ser Glu	Tyr ₃₅₀ Gln Leu
Pro Tyr Val	Leu ₃₅₅ Gly Ser Ala His	Gln ₃₆₀ Gly Cys Leu	Pro ₃₆₅ Pro Phe Pro
Ala Asp ₃₇₀ Val Phe Met Ile	Pro ₃₇₅ Gln Tyr Gly Tyr	Leu ₃₈₀ Thr Leu Asn Asn	
Gly ₃₈₅ Ser Gln Ala Val	Gly ₃₉₀ Arg Ser Ser Phe	Tyr ₃₉₅ Cys Leu Glu Tyr	Phe ₄₀₀
Pro Ser Gln Met	Leu ₄₀₅ Arg Thr Gly Asn	Asn ₄₁₀ Phe Gln Phe Thr	Tyr ₄₁₅ Thr
Phe Glu Asp	Val ₄₂₀ Pro Phe His Ser	Ser ₄₂₅ Tyr Ala His Ser	Gln ₄₃₀ Ser Leu

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445
 Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
 450 455 460
 Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
 465 470 475 480
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
 485 490 495
 Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
 500 505
 Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
 515 520 525
 Lys Asp Asp Glu Glu Arg Phe Phe Pro Val Thr Gly Ser Cys Phe Trp
 530 535 540
 Gln Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
 545 550 555 560
 Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
 565 570 575
 Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
 580 585 590
 Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
 705 710 715 720
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 164
 <211> 735
 <212> PRT
 <213> vp1, clone hu.35
 <400> 164
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 165
 <211> 3161
 <212> DNA
 <213> new AAV serotype, clone hu 136.1

<400> 165

gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt	60
ccattcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc	120
aaggtcatgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa	180
tgtaagtcct cggcccagat agaccgact cccgtgattg tcacctcaa caccaacatg	240
tgcgccgtga ttgacgggaa ctcaacgacc ttcgagcacc agcagccgtt gcaagaccgg	300
atgttcaa at ttgaactcac ccgccgtctg gatcatgact ttgggaagggt caccaagcag	360
gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgagggtga gcatgaattc	420
tacgtcaaaa aggggtggagc caagaaaaga cccgccccca gtgacgcaga tataagtga	480
cccaaacggg cgcgcggtc agttgcgcag ccacgcagct cagacgcgga agcttcgatc	540
aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg	600
tttccctgca gacaatgcga gagaatgaat caaaattcaa atatctgctt cactcacgga	660
cagaaggact gtttagatg ctttcccggtg tcagaatctc aaccctgttc tgtcgtcaaa	720
aaggcgtatc agaaactttg ctacattcat catatcatgg gaaagggtgcc agacgcttgc	780
actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt	840
ttaatcaggt atggctgccg atggttatct tccagattgg ctcaaggaca ctctctctga	900
aggaataaga cagtgggtga agctcaaacc tggccccacca ccaccaaagc ccgcagagcg	960
gcataaggac gacagcgggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa	1020
cggactcgac aaggagagc cggccaacga ggcagacgcc gcggccctcg agtacgacaa	1080
ggcctacgac cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga	1140
cgcgaggttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc	1200
agtcttccag gcgaaaaaga ggggtcttga acctctgggc ctggttgagg aacctgttaa	1260
gacggctccg gaaaaaaga ggcgggtaga gcaactctct gtggagccag actcctctc	1320
gggaacagga aaagcgggcc agcagcctgc gagaaagaga ttgaattttg gtcagactgg	1380
agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctgg	1440
tctgggaact aatacagtg ctacaggcag tggcgaccca atggcagaca ataacgagg	1500
cgccgacgga gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcga	1560
cagagtcatc accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta	1620
caagcagatc tccagccaat caggagccag caacgacaac cactactttg gctacagcac	1680
cccttggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca	1740
aagactcatc aacaacaact ggggatttcg gcccaagaga ctcaacttca agctctttaa	1800
cattcaagtc aaggagggtca cgagaatga cggtagcag acgattgcca ataaccttac	1860
cagcacggtt cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc ccggctcggc	1920
gcatcaagga tgcttccgc cgttcccgag agacgtcttc atggtgccac agtatggata	1980
cctcacctg aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta	2040
ctttccttct cagatgcttc gtaccggaaa caactttacc ttcagctaca ctttgagga	2100
tgttcctttc cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct	2160
catcgaccag tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca	2220
gtccaggctt cagttttctc aggcgggagc aagtgcatt cgggaccagt ctaggaaactg	2280
gcttcttggg ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa	2340
cagtgaatac tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt	2400
gaatccgggc ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag	2460
cggggttctc atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg	2520
catgattaca gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg	2580
ttctgtatct accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac	2640
acaaggcgtt ctccagcgca tggcttgcca ggacagagac gtgcacctgc aggggcctat	2700
ctgggcaaag attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt	2760

tggacttaaa caccctcctc cacagattct catcaagaac accccggtac ctgcaaattcc 2820
 ttcgaccacc ttcagtgctg caaagtttgc ttccttcac acacagtatt ccacagggca 2880
 ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga 2940
 gatccagtac acttccaact acaacaaatc tgttaattgt gactttactg tggacactaa 3000
 tgggtgtgat tcagagcctc gcccattgg caccagatac ctgactcgta atctgttaatt 3060
 gcttggttaat caataaacg ttttaattcgt ttcagttgaa ctttggtctc tgcgaagggc 3120
 gaattcggtt aaaccctgca ggactagtcc ctttagtgag g 3161

<210> 166
 <211> 3162
 <212> DNA
 <213> new AAV serotype, clone hu 140.1

<400> 166
 gaattgaatt tagcggccgc gaattcgccc ttcgcagaga ccaaagttca actgaaacga 60
 attaaacggt ttattgatta acaagcaatt acagattacg agtcagggtat ctggtgccaa 120
 tggggcgagg ctctgaatac acgccattag tgtccacagt aaagtccaca ttaacagact 180
 tgttgtagt ggaagtgtac tgaatttcgg gattccagcg tttgctgttt tccttctgca 240
 gctccactc gatctccacg ctgacctgtc ccgtggagta ctgtgtgatg aagggaagcaa 300
 actttgccgc actgaagggt gtcgaaggat tcgcagggtac cggggtgttc ttgatgagaa 360
 tctgtggagg aggggtgtta agtccgaatc caccatgag gggagagggg tgaaaatgtc 420
 cgtccgtgtg tggaaatctt gccagatgg gccctgaag gtacacatct ctgtcctgcc 480
 agaccatgcc tggagaacg cttgtgtgt tgacatctgc ggtagctgct tgtctgttgc 540
 ctctctggag gttggtgat acagaaccgt actgctccgt agccacggga ttggttgtcc 600
 tgatttcctc ttcgtctgta atcatgacct tttcaatgtc cacatttgtt ttctctgagc 660
 cttgcttccc aaagatgaga accccgctct gaggaaaaaa cttttcttca ttgtccttgt 720
 ggcttgccat ggcggggccc ggattcacca gagagtctct gccattgagg tggtaacttg 780
 tagctccagt ccacgagtat tctgtgtgt tgttatccgc agatgtcttt gatactcgct 840
 gctggcggtg acaggggtcca ggaagccagt tcctagactg gtcccgaatg tctactgctc 900
 cggcctgaga aaactgaagc cttgactgcg tgggtggttc acttgagtg tttgttgtgc 960
 tcaagtaata cagggtactg tcgatgagag gattcatgag acggtccaga ctctggctgt 1020
 gagcgtagcc gctgtggaaa ggaacgtcct caaaagtgtg gctgaaggta aagtgtttc 1080
 cggtagcgag catctgagaa ggaaagtact ccaggcagta aaatgaagag cgtcctactg 1140
 cctgactccc gttgttcagg gtgaggtatc catactgtgg caccatgaag acgtctgctg 1200
 ggaacggcgg gaggcacctc tgatgcgccc agccgaggac gtacgggagc tggtaactccg 1260
 agtcagtaaa cacctgaacc gtgctggtaa ggttattggc aatcgtcgtc gtaccgtcat 1320
 tctgcgtgac ctctttgact tgaatgttaa agagcttgaa gttgagtctc ttgggtcgga 1380
 atccccagtt gttgttgatg agtctttgcc agtcacgtgg tgaaaagtgg cagtggaaatc 1440
 tgttgaagtc aaaatacccc caaggggtgc tgtagccaaa gtagtgattg tcgttcgagg 1500
 ctctgattg gctggaaaatt tgtttgtaga ggtggtgtt gtaggtgggc agggcccagg 1560
 ttcgggtgct ggtggtgatg actctgtcgc ccattcatgt ggaatcgcaa tgccaatttc 1620
 ccgaggaatt acccactccg tcggcgccct cgttattgtc tgccattggt gcgccactgc 1680
 ctgtagccat cgtattagtt cccagaccag agggggctgc tgggtggctgt ccgagaggct 1740
 gggggctcagg tactgagtct gcgtctccag tctgacaaa attcaatctt tttcttgca 1800
 gctgctggcc cgctttccg gttcccagg aggagctctg ctccacagga gagtgtctta 1860
 ccggcctctt ttttcctgga gccgtcttga cagggtcccc aaccaggccc agaggttcaa 1920
 gaacctctt tttcgcttg aagactgtc gtccgaggtt gccccaaaa gacgtatctt 1980
 cttaaggcg ctccctgaac tccgcgtcgg cgtggttcta cttgaggtac ggggtgtctc 2040
 cgctgtcgag ctgcccgtcg taggctttgt cgtgctcgag ggccgcggcg tctgcctcgt 2100

tgaccggctc tcccttgtcg agtccgttga aggggtccgag gtacttgtac ccaggaagca 2160
 caagaccct gctgtcgtcc ttatgccgtt ctgcgggctt tgggtgggtt gggccagggt 2220
 tgagcttcca cactgtctt attccttcag agagagtgtc ctgagccaa tctggaagat 2280
 aaccatcggc agccatacct gatttaaattc atttattgtt caaagatgca gtcattcaaa 2340
 tccacattga ccagatcgca ggcagtgcga gcgtctggca cttttcccat gatatgatga 2400
 atgtagcaca gtttctgata cgcctttttg acgacagaaa cgggttgaga ttctgacacg 2460
 ggaaagcact ctaaacagtc tttctgtccg tgagtgaagc agatatttga attctgattc 2520
 attctctcgc attgtctgca gggaaacagc atcagattca tgcccacgtg acgagaacat 2580
 ttgttttggg acctgtctgc gtagtgtatc gaagcttccg cgtctgacgt cgatggctgc 2640
 gcaactgact cgcgcacccg tttgggtcga cttatatctg cgtcactggg ggcgggtctt 2700
 ttcttggtc cacccttttt gacgtagaat tcatgtcca cctcaaccac gtgatctttt 2760
 gcccaccgga aaaagtcttt gacttcctgc ttggtgacct tcccaaagtc atgatccaga 2820
 cggcgggtga gttcaaatgt gaacatccgg tcttgcacg gctgctggtg ttcgaagggtc 2880
 gttgagttcc cgtcaatcac ggcgcacatg ttggtgttgg aggtgacgat cacgggagtc 2940
 ggggtctatct gggccgagga cttgcatttc tgggtccacgc gcaccttgct tcttccgaga 3000
 atggcttttg ccgactccac gaccttggcg gtcattctcc cctcctcca ccagatcacc 3060
 atcttgtcga cacagtcgtt gaagggaag ttctcattgg tccagttgac gcagcaaggg 3120
 cgaattcgtt taaacctgca ggactagtc ctttagtgag gg 3162

<210> 167
 <211> 3164
 <212> DNA
 <213> new AAV serotype, clone hu 140.2

<400> 167
 gcgaattgaa tttagcggcc gcgaattcgc ccttcgcaga gaccaaagtt caactgaaac 60
 gaattaaacg gtttattgat taacaagcaa ttacaaatta cgagtcaggt atctgggtgcc 120
 aatggggcga ggctctgaat acacgccatt agtgtccaca gtaaagtcca cattaacaga 180
 cttgtttagt ttggaagtgt actgaatttc gggattccag cgtttgctgt tttccttctg 240
 cagctccac tcgatctcca cgctgacctg tcccgtggag tactgtgtga tgaaggagc 300
 aaactttgcc gactgaagg tggcgaagg attcgcaggt accgggggtg tcttgatgag 360
 aatctgtgga ggagggtgt taggtccgaa tccacctatg aggggagagg ggtgaaaatg 420
 tccgtccgtg tgtggaatct ttgccagat gggccctga aggtacacat ctctgtcctg 480
 ccagaccatg cctggaagaa cgccttgtgt gttgacatct gcggtagctg cttgtctgtt 540
 gcctctctgg aggttggtag atacagaacc atactgtcc gtagccacgg gattggtgt 600
 cctgatttcc tcttctgtctg taatcatgac cttttcaatg tccacatttg ttttctctga 660
 gccttgcctt ccaaagatga gaaccccgct ctgaggaaaa aacttttctt cattgtcctt 720
 gtggcttgcc atggccgggc ccggattcac cagagagtct ctgccattga ggtggactt 780
 ggtagctcca gtccacgagt attcactgtt gttgttatcc gcagatgtct ttgatactcg 840
 ctgctggcgg taacagggtc caggaagcca gttcctagac tgggtccgaa tgtcactcgc 900
 tccggcctga gaaaactgaa gccttgactg cgtgggtggt ccacttggag tgtttgttgt 960
 gctcaagtaa tacagggtact ggtcgatgag aggttcatg agacggtcca gactctggct 1020
 gtgagcgtag ctgtgtgga aaggaaagtc ctcaaaagtg tagctgaagg taaagtgttt 1080
 tccggtacgc agcatctgag aaggaaagta ctccgggcag taaaatgaag agcgtcttac 1140
 tgcttgactc ccgttgcctc ggggtgagga tccatactgt ggcaccatga agacgtctgc 1200
 tgggaacggc gggaggcatc cttgatgcgc cgagccgagg acgtacggga gctgggtactc 1260
 cgagtcagta aacacctgaa ccgtgctggt aaggttattg gcaatcgtcg tctgaccgtc 1320
 attctgcgtg acctctttga cttgaatgtt aaagagcttg aagttgagtc tcttgggtcg 1380
 gaatccccag ttgttgttga tgagtctttg ccagtcacgt ggtgaaaagt ggcagtggaa 1440

```

tctgttgaag tcaaaataacc cccaaggggt gctgtagcca aagtagtgat tgtcgttcga 1500
ggctcctgat tggttgaaa tttgtctgta gaggtggtg ttgtagggtg gcagggccca 1560
ggttcgggtg ctggtggtga tgactctgtc gcccatccat gtggaatcgc aatgccgatt 1620
tcccagaggaa ttaccactc cgtcggcgcc ctcgttattg tctgccattg gtgcgccact 1680
gcctgtagcc atcgtattag tttccagacc agagggggct gctggtggct gtccgagagg 1740
ctgggggtca ggtactgagt ctgcgtctcc agtctgacca aaattcaatc tttttcttgc 1800
aggctgctgg cccgcctttc cggttcccga ggaggagtct ggctccacag gagagtgtct 1860
taccggcctc ttttttcccg gagccgtctt aacagggtcc ccaaccaggc ccagagggtc 1920
aagaaccctc tttttcgcct ggaagactgc tcgtccgagg ttgccccaa aagacgtatc 1980
ttctttaagg cgctcctgaa actccgcgtc ggcgtggtg tacttgagg acgggttgtc 2040
tccgctgtcg agctgccggt cgtaggcttt gtcgtgtctg agggccgcgg cgtctgcctc 2100
gttgaccggc tctcccttgt cgagtcctgt gaagggtccg aggtacttgt acccaggaag 2160
cacaagacc ctgctgtcgt cttatgccc cctcgcggc tttggtggtg gtgggccagg 2220
tttgagcttc caccactgtc ttattcctt agagagagt tcctcgagcc aatctggaag 2280
ataaccatcg gcagccatac ctgatttaaa tcatttattg ttcaaagatg cagtcatcca 2340
aatccacatt gaccagatcg caggcagtgc aagcgtctg cacccttccc atgatatgat 2400
gaatgtagca cagtttctga tacgccttt tgacgacaga aacgggttga gattctgaca 2460
cgggaaagca ctctaaacag tctttctgtc cgtgagtga gcagatatt gaattctgat 2520
tcattctctc gcattgtctg cagggaaca gcatcagatt catgcccacg tgacgagaac 2580
atttgttttg gtacctgtct gcgtagtga tcgaagcttc cgcgtctgac gtcgatggct 2640
gcgcaactga ctcgcgcacc cgtttgggct cacttatatc tgcgtcactg ggggcgggtc 2700
ttttcttggc tccacccttt ttgacgtaga attcatgtc caccctcaac acgtgatcct 2760
ttgcccaccg gaaaaagtct ttgacttcct gcttggtgac cttcccaaag tcatgatcca 2820
gacggcgggt gagttcaaat ttgaacatcc ggtcttgcaa cggctgctg tgttcgaagg 2880
tcgttgagtt cccgtcaatc acggcgaca tgttggtgtt ggagggtgac atcacgggag 2940
tcgggtctat ctgggcccag gacttgcatt tctggtccac gcgcacctg cttcctccga 3000
gaatggcttt ggccgactcc acgaccttgg cggtcattt cccctcctcc caccagatca 3060
ccatcttgtc gacacagtgc ttgaaggga agttctcatt ggtccagttg acgcagcaag 3120
ggcgaattcg tttaaacctg caggactagt cccttttagt aggg 3164

```

<210> 168

<211> 3159

<212> DNA

<213> new AAV serotype, clone hu 147.2

<400> 168

```

gattgattta gcggccgcga attcgccctt gctgcgtcaa ctggaccaat gagaactttc 60
ccttcaacga ttgctcgac aagatggtga tctggtggga ggagggaag atgaccgcca 120
aggctcgtga gtcggccaaa gccattctcg gaggaagcaa ggtgctgtg gacaaaaagt 180
gcaagtcttc ggcccagatc gaccgactc ccgtgatcgt caccctcaac accaaccatgt 240
gcgccgtgat tgatggaac tcaacgacct tcgagacca gcagccgtg caagaccgga 300
tgttcaaatt tgaacttacc cgccgtctgg atcatgactt tggaaagggt accaagcagg 360
aagtgaaga ctttttccgg tgggcaaagg atcacgtggt tgagggtggag catgagttct 420
acgtcaaaaa ggttgagacc aaaaaagac ccgccccag tgacgcagat ataagtgagc 480
ccaaacgggc gcgcgagtca gttgcgcagc catcgacgtc agacgcggaa gcttcgatca 540
actacgcgga caggtaacaa acaaatgtt ctcgtcacgt gggcatgaat ctgatgctgt 600
ttccctgcag acaatgcgag agaattgaatc agaattcaaa tatctgcttc actcacggac 660
agaaagactg tccatagtgc tttcccgtgt cagaatctca acccgtttct gtcgtcaaaa 720
aggcgtatca gaaactgtgc tacattcatc acatcatggg aaagggtgcca gacgcttgca 780

```

ctgcttgca cctggtcaat gtggatttgg atgactgcat ctctgaacaa taaatgattt 840
 aaatcaggta tggctgccga tggttatctt ccagattggc tcgaggacac tctctctgaa 900
 ggaataagac agtgggtggaa gctcaaacct ggcccaccac caccaaagcc cgcagagcgg 960
 cataaggacg acagcagggg tcttgtgctt cctggataca agtacctcgg acccttcaac 1020
 ggactcgaca agggagagcc ggtcaacgag gcagacgccg cggccctcga gcacgacaag 1080
 gcctacgacc ggcagctcga cagcggagac aaccctgacc tcaagtacaa ccacgccgac 1140
 gcggagtttc aggagcgcct taaagaagat acgtcttttg ggggcaacct cggacgagca 1200
 gtcttccagg cgaaaaagag ggttcttgaa cctctgggccc tggttgagga acctgttaag 1260
 acggctcccg gaaaaaagag gccggtagag cactctcctg tggagccaga ctctcctcctg 1320
 ggaaccggaa aagcgggcaa ccagcctgca agaaaaagat tgaatttcgg tcagactgga 1380
 gacgcagact ccgtacctga cccccagcct ctcggacagc caccagcatc cccctctggt 1440
 ctgggaacta atacgatggc tacaggcagt ggcgcaccaa tggcagacaa taacgagggc 1500
 gccgcaggag tgggtaattc ctcgggaaat tggcattgag attccacatg gatgggagac 1560
 agagtcgtca ccaccagcac ccgcacctgg gccctgccc cctacaacaa ccacctctac 1620
 aagcagattt ccagccaatc aggagccagc aacgacaacc actacttttg ctacagcacc 1680
 ccttgggggt attttgactt caacagattc cactgccact tttcgccacg cgactggcag 1740
 agactcatca acaacaactg gggattccgg cccaaaagac tcaacttcaa gctgtttaac 1800
 attcaagtca aggaggtcac gcagaatgac ggtacgacga cgattgccaa taaccttacc 1860
 agcacggttc aggtgtttac tgacttggag taccagctcc cgtacgtcct cggctcggcg 1920
 catcaaggat gcctcccggc gttcccagca gacgtcttca tggtgccaca gtatggatac 1980
 ctcaccctga acaacgggag tcaggcggta ggacgctctt ccttttactg cctggagtac 2040
 tttctttctc agatgcttcg caccggaaac aactttacct tcagctacac ttttgaagac 2100
 gttcctttcc acagcagcta cgctcacagt caaagtctgg accgtctcat gaatcctctc 2160
 atcgaccagt acctgtatta cttgagcaga acaaacactc caagcggaa cactacgcag 2220
 tccaggcttc agttttctca ggccggagcg agtgacattc gggaccagtc taggaactgg 2280
 cttcctggac cctgttaccg ccagcagcga gtatcaaaga cagctgcgga taacaacaac 2340
 agtgaatact cgtggactgg agctaccaag taccacctca atggcagaga ctctctggtg 2400
 aatccgggccc cggccatggc cagccacaag gacgatgaag aaaagttttt tcctcaaagc 2460
 ggggttctca tctttgggaa gcaaggctca gagaaaacaa atgtggacat tgaaaaggtc 2520
 atgattacag acgaagagga aatcaggacc accaatcccg tggctacgga gcagtatggt 2580
 tctgtatcta ccaacctcca gagcggcaac acacaagcag ctacctcaga tgtcaacaca 2640
 caaggcggtc ttccaggcat ggtctggcag gacagagacg tgtacctgca ggggcccatc 2700
 tgggcaaaaa ttccacacac ggacggacat tttcacccct ctcccctcat gggcggattt 2760
 ggacttaaac accctcctcc acagattctc attaagaata ccccggatcc tgcgaatcct 2820
 tcgaccacct tcagcgcggc aaagtgtgct tccttcatca cacagtattc cacggggcag 2880
 gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaatcccgaa 2940
 attcagtaca cttccaacta caacaaatct gttaatgtgg actttactgt ggacactaat 3000
 ggggtgtatt cagagcctcg ccctattggc accagatacc tgactcgtaa tctgtaattg 3060
 cttgttaatc aataaaccgt ttaattcggt tcagttgaac tttggtctct gcgaagggcg 3120
 aattcgttta aacctgcagg actagtcctt ttagtgagg 3159

<210> 169
 <211> 3156
 <212> DNA
 <213> new AAV serotype, clone hu 147.3

<400> 169
 cgattgaatt tagcggccgc gaattcgccc ttgctgcgtc aacggaccaa tgagaacttt 60
 cccttcaacg attgcgtcga caagatgggt atctgggtggg aggaagggaaa gatgaccgcc 120

aaggtcgtgg	agtcggccaa	agccattctc	ggaggaagca	aggtgcgtgt	ggacaaaaag	180
tgcaagtctt	cggcccagat	cgacccgact	cccgtgatcg	tcacctcaa	caccaacatg	240
tgcgccgtga	ttgatggaaa	ctcaacgacc	ttcgagcacc	agcagccgtt	gcaagaccgg	300
atgttcaaat	ttgaacttac	ccgccgtctg	gatcatgact	ttggaaagg	caccaagcag	360
gaagtgaag	actttttccg	gtgggcaaag	gatcacgtgg	ttgaggtgga	gcatgagttc	420
tacgtcaaaa	aggggtggagc	caaaaaaaga	cccgcacca	gtgacgcaga	tataagtgag	480
cccaaaccgg	cgcgcgagtc	agttgctcag	ccatcgacgt	cagacgcgga	agcttcgatc	540
aactacgcgg	acaggtacca	aaacaaatgt	tctcgtcacg	tgggcatgaa	tctgatgctg	600
tttccttcca	gacaatgcga	gcgaatgaat	cagaattcaa	atatctgctt	cactcacgga	660
cagaaagact	gttttagagt	ctttcccgtg	tcagaatctc	aacccgtttc	tgtcgtcaaa	720
aaggcgtatc	agaaactgtg	ctacattcat	cacatcatgg	gaaagggtgc	agacgcttgc	780
actgcttgcg	acctgggtcaa	tgtggatttg	gatgactgca	tctctgaaca	ataaatgatt	840
taaatcagg	atggctgcgg	atggttatct	tccagattgg	ctcaggagaca	ctctctctga	900
aggaataaga	cagtgggtgga	agctcaaacc	tggccacca	ccaaagcccg	cagagcggca	960
taaggacgac	agcaggggtc	ttgtgcttcc	tggatacaag	tacctcggac	ccttcaacgg	1020
actcgacaag	ggagagccgg	tcaacgaggg	agacgcgcgg	gccctcgagc	acgacaaggc	1080
ctacgaccgg	cagctcgaca	gcggagacaa	cccgtacctc	aagtacaacc	acgccgacgc	1140
ggagtttcag	gagcgcttta	aagaagatac	gtcttttggg	ggcaacctcg	gacgagcagt	1200
cttcaggcg	aaaaagagg	ttcttgaacc	tctgggcctg	gttgaggaa	ctgttaagac	1260
ggctccggga	aaaaagagg	ccgtagagca	ctctcctgtg	gagccagact	cctcctcggg	1320
aaccggaaaa	gcgggcaacc	agcctgcaag	aaaagattg	aatttcgggtc	agactggaga	1380
cgcgactctc	gtacctgacc	cccagcctct	cggacagcca	ccagcagccc	cctctggtct	1440
gggaactaat	acgatggcta	caggcagtgg	cgcaccaatg	gcagacaata	acgagggcgc	1500
cgacggagtg	ggtaattcct	cgggagattg	gcattgcgat	tccacatgga	tgggcgacag	1560
agtcacacc	accagcacc	gcacctgggc	cctgcccacc	tacaacaacc	acctctacaa	1620
gcagatttcc	agccaatcag	gagccagcaa	tgacaaccac	tactttggct	acagcacccc	1680
ttgggggtat	tttgacttca	acagattcca	ctgccacttt	tcgccacgcg	actggcagag	1740
actcatcaac	aacaactggg	gattccggcc	caaagactc	aacctcaagc	tgtttaacat	1800
tcaagtcaag	gaggtcacgc	agaatgacgg	tacgacgacg	attgccaata	accttaccag	1860
cacggttcag	gtgtttactg	acttgagta	ccagctcccg	tacgtcctcg	gctcggcgca	1920
tcaaggatgc	ctccgcgcgt	tcccagcaga	cgtcttcatg	gtgccacagt	atggatacct	1980
caccctgaac	aacgggagtc	aggcggtagg	acgctcttcc	ttttactgcc	tggagtactt	2040
tccttctcag	atgcttcgta	ccggaaacaa	ctttaccttc	agctacactt	ttgaagacgt	2100
tcctttccac	agcagctacg	ctcacagtca	aagtctggac	cgtctcatga	atcctctcat	2160
cgaccagtac	ctgtattact	tgagcagaac	aaacactcca	agcggaaacca	ctacgcagtc	2220
caggcttcag	ttttctcagg	ccggagcgag	tgacattcgg	gaccagtcta	ggaactggct	2280
tcctggacc	tgttaccgcc	agcagcgagt	atcaaagaca	gctgcggata	acaacaacgg	2340
tgaatactcg	tggactggag	ctaccaagta	ccacctcaat	ggcagagact	ctctggtgaa	2400
tccgggcccc	gccatggcca	gccacaagga	cgatgaagaa	aagttttttc	ctcaaagcgg	2460
ggttctcatc	tttgggaagc	aaggctcaga	gaaaacaaat	gtggacattg	aaaagggtcat	2520
gattacagac	gaagaggaaa	tcaggaccac	caatcccgtg	gctacggagc	agtatgggtc	2580
tgtatctacc	aacctccaga	gcggcaacac	acgagcagct	acctcagatg	tcaacacaca	2640
aggcgttctt	ccaggcatgg	tctggcagga	cagagacgtg	tacctgcagg	ggcccatctg	2700
ggcaaaaatt	ccacacacgg	acggacattt	tcacccctct	cccctcatgg	gcggatttgg	2760
acttaaacac	cctcctccac	agattctcat	taagaatacc	ccggtacctg	cgaatccttc	2820

gaccactttc agcgcggtcaa agtttgcttc cttcatcaca cagtattcca cggggcaggt 2880
 cagcgtggag atcagagtggg agctgcagaa ggagaacagc aaacgctgga atccccgaaat 2940
 tcagtacact tccaactaca acaaatctgt taatgtggac ttactgtgg acactaatgg 3000
 ggtgtattca gagcctcgcc ctattggcac cagatacctg actcgtaatc tgtaattgct 3060
 tgtaaatcaa taaaccgttt aattcgtttc agttgaactt tggctctctgc gaagggcgaa 3120
 ttcgtttaaa cctgcaggac tagtcctttt agtgag 3156

<210> 170
 <211> 3158
 <212> DNA
 <213> new AAV serotype, clone hu 161.10

<400> 170
 gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60
 cttttcaatg attgcgtcga caagatggtg atctgggtggg aggagggaaa gatgaccgcc 120
 aaggctcgtg agtcggccaa agccattctc ggaggaagca aggtgcgcgc ggaccagaaa 180
 tgcaagtctt cggcccagat agaccgcact cccgtgattg tcacctcaa caccaacatg 240
 tgcgcctgta ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg 300
 atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag 360
 gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420
 tacgtcaaaa aggggtggagc taagaaaaga cccgccccca gtgacgcaga tataagtgag 480
 cccaaacggg cgcgcgagtc agttgcgcag ccacgcagct cagacgcgga agcttcgatc 540
 aactacgcgg gcaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600
 tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga 660
 cagaaagact gtttagagtg ctttcccggt tcagaatctc aaccctgttc tgcgtcctg 720
 aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780
 actgcctgct atctgggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840
 taaatcaggt atggctgccc atggttatct tccagattgg ctgaggaca ctctctctga 900
 aggaataaga cagtgggtga agctcaaacc tggccacca ccaccaagc ccgcagagcg 960
 gcataaggac gacagcaggg gtcttgtgct tcttgggtac aagtacctcg gaccttcaa 1020
 cggactcgac aaggggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa 1080
 ggcttacgac cggcagctcg acagcggaga caaccctac ctcaagtaca accacgccga 1140
 cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200
 agtctttccg gcaaaaaaga gggttcttga acctctgggc ctgggtgagg aacctgttaa 1260
 aacggctccg ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctctc 1320
 gggaaaccga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg 1380
 agacgcagac tccgtacctg acccccagcc tctcgacag ccaccagcag cccctctggt 1440
 tctgggatct actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg 1500
 tgccgatgga tggggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga 1560
 cagagtcata accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta 1620
 caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac 1680
 cccctggggg tatttttgact tcaacagatt ccaactgccac ttttcaccac gtgactggca 1740
 aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa 1800
 cattcaagtc aaagaggtca cgcagaatga cggtagcagc acgattgcca ataacttac 1860
 cagcacggtt caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc 1920
 gcatcaagga tgcttccgcg cgtttccagc ggacgtcttc atgggtccac agtatggata 1980
 cctcaccctg aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta 2040
 ctttctctct cagatgctgc gtaccggaaa caactttcaa ttcagctaca cttttgaaga 2100
 cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct 2160

ggctgacag: taccctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca 2220
 gtctcggcta ctgttttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg 2280
 gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacy acaacaacaa 2340
 cagcaacttt ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg 2400
 taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca 2460
 tggaaaccctt atatttggtg aacaaggaaac aaatgccaac gacgcggatt tggaaaatgt 2520
 catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg 2580
 aactgtatca aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatca 2640
 ccaaggagcg ttacctggta tgggtgggca ggatcgagac gtgtacctgc agggacccat 2700
 ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactga tgggagggtt 2760
 tggactcaaa caccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc 2820
 tccccaaaac ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca 2880
 ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacygt ggaatcccga 2940
 aattcagtac acttccaaact acaacaaatc tgtaaatgtg gactttactg tggacactaa 3000
 tgggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060
 gcttgtaaat caataaaccg ttaattcgt ttcagttgaa ctttgggtctc tgcgaagggc 3120
 gaattcggtt aaacctgcag gactagtccc tttagtga 3158

<210> 171
 <211> 3167
 <212> DNA
 <213> new AAV serotype, clone hu 172.1

<400> 171
 attgaattta gcggccgcga attcgccctt cgcagagacc aaagtccaac tgaaacgaat 60
 taaacgggtt attgattaac aagcaattac agattacgag tcaggtagct ggtgccaatg 120
 gggcgaggct ctgaatacac accattagtg tccacagtaa agtccacatt aacagatttg 180
 ttgtagtgg aagtgtactg aatctcggga ttccagcgtt tgctgttctc cttctgcagc 240
 tcccactcga tctccacgct gacctgcccc gtggagtact gtgtaatgaa ggaagcaaac 300
 tttgccgcac tgaaggtagt cgaaggattc gcaggtagcg ggggtttctt gatgagaatc 360
 tgcgggggag ggtgtttaag tccgaatccg cccatgaggg gagaggggtg aaaaagtccg 420
 tccgtgtgtg gaatctttgc ccagatgggc cctgcaggt acacgtctct gtccctgccac 480
 accatgcctg gaagaacgcc ttgtgtgttg acatctgagg tagctgcttg tgtgttgccg 540
 ctctggaggt tggtagatac agaaccatac tgctccgtag ccacgggatt ggtggtcctg 600
 atttcctctt cgtctgtaat catgaccttt tcaatgtcca cattagtttt tcccaggtct 660
 tgttttccaa agatgagaac cccgctctga ggaaaaaact tttcttcatc gtccctgttg 720
 ctggccatgg ccgggcccg attcaccaga gagtctcttc cattaagggtg gtacttggtg 780
 gctccagtcc acgagtattc actgttgttg ttatccgcag atgtctttga tactcgctgc 840
 tggcggtaac aggggtccagg aagccagttc ctgactgggt cccgaatgtc acttgctccg 900
 gcctgagaaa actgaagcct tgactgctg gtgtgtccgc ttggagtgtt tgttctgctc 960
 aagtaataca ggtactggtc gatgagagga ttcatgagac ggtccaaact ctggctgttg 1020
 gcgtagctgc tgtggaaagg aacgtcctca aaggtgtgac tgaaggtaaa gttgtttccg 1080
 gtacgcagca tctgagaagg aaagtactcc aggcagtaaa atgaagagcg tctactgcc 1140
 tgactcccgt tgttcagggt gaggtatcca tactgtggca ccatgaagac gtctgctggg 1200
 aacggcggga ggcattcctg atgcgccgag ccgaggacgt acgggagctg gtactccgag 1260
 tcagtaaaaca cctgaaccgt gctggtaagg ttattggcaa tcgtcgtcgt accgtcattc 1320
 tgcgtgacct ccttgacttg aatgttaaag agcttgaagt tgagtctttt gggccggaat 1380
 ccccaattgt tgttgatgag tctttgccag tcacgtggcg aaaagtggca gtggaatctg 1440
 ttgaagtcaa aataccccca aggggtgctg tagccaaagt agtgggtgtc gtttgaggct 1500

cctgattggc tggaaatctg cttgtagagg tgggtgttgt aggtgggcag agcccagggtg 1560
 cggtgtctgg tggatgatgac tctgtcgccc atccatgtgg aatcgcaatg ccaatttccc 1620
 gaggaattac cactccgctc ggcgccctcg ttattgtctg ccattggtgc gccactgcct 1680
 gtagccatcg tattagttcc cagaccagag ggggctgtg gtggtgttcc gagaggctgg 1740
 gggtcaggta cggagtctgc gtctccagtc tgaccgaaat tcaatctctt tcttgaggc 1800
 tgctggccc cttttccggt tcccaggag gagtctggct ccgcaggaga gtgctctacc 1860
 ggcctctttt tcccggagc cgtcttaaca gggtcctcaa ccaggcccag aggttcaaga 1920
 accctctttt tcgcttgaa gactgtctgt ccgagggtgc cccaaaaga cgtatcttct 1980
 ttaagacgct cctggaactc cgcgtcggcg tgggtgtact tggggtacgg gttgtctccg 2040
 ctgtcgagct gccggctgta ggccttgtcg tgctcgaggg ccgcggcgct tcctctgttg 2100
 accggtcttc cttgtcgag tccgttgaag ggtccaagg acttgtaacc aggaagcaca 2160
 agaccctgc tgcgtctct atgccgtct gcgggctttg tgggtggtgg gccagggttg 2220
 agcttcacc actgtcttat tccttcagag agagtgtcct cgagccaatc tggagataa 2280
 ccacggcag ccatacctga tttaaatcat ttattgttca gagatgcagt catccaaatc 2340
 cacattgacc agatcgcaag cagtgcagc gtctggcacc tttcccatga tatgatgaat 2400
 gtagcacagt ttctgatacg cttttttgac gacagaaacg ggttgagatt ctgacacggg 2460
 aaagcactct aaacagtctt tctgtccgtg agtgaagcag atatttgaat tctgattcat 2520
 tctctcgcat tgtctgcagg gaaacagcat cagattcatg cccacgtgac gagaacattt 2580
 gttttggtac ctgtccgct agttgattga agcttccgc tctgacgtcg atggctgctc 2640
 aactgactcg cgcgccctt tgggtcact tatatctgcg tctactgggg cggtctttt 2700
 tttggtcca cctttttga cgtagaattc atgtctacc tcaaccacgt gatcctttgc 2760
 ccaccgaaa aagtctttga cttctgtctt ggtgacctt ccaaagtcag gatccagacg 2820
 gcgggtgagt tcaaatttga acatccggtc ttgcaacggc tgctggtgtt cgaaggctgt 2880
 tgagtcccc tcaatcactg cgcacatgtt ggtgttgag gtgacaatca cgggagtcgg 2940
 gtctatctgg gccgaggact tgcatttctg gtccacgcgc accttgcttc ctccgagaat 3000
 ggctttggcc gactccacga cttggcgggt catcttcccc tcctccacc agatcaccat 3060
 cttgtcgacg caatcattga aaggaaagt ctcatgtgtc cagttgacgc agccgtagaa 3120
 agggcgaatt cgtttaaacc tgcaggacta gtcccttag tgagggt 3167

<210> 172
 <211> 3161
 <212> DNA
 <213> new AAV serotype, clone hu 172.2

<400> 172
 aattgaattt agcggccgcg aattcgccct tcgcagagac caaagttcaa ctgaaacgaa 60
 ttaaacggtt tattgattaa caagcaatta cagattacga gtcaggatc tgggtgccaat 120
 ggggcgaggc tctgaataca caccattagt gtccacagta aagtccacat taacagattt 180
 gttgtagttg gaagtgtact gaatctcggg attccagcgt ttgctgttct cttctgcag 240
 ctcccactcg atctccacgc tgacctgccc cgtggagtac tgtgtaatga aggaagcaaa 300
 ctttgccgca ctgaaggtag tcgaaggatt cgcaggatc ggggtgttct tgatgagaat 360
 ctgcggggga ggggtgttaa gtccgaatcc gcccatgagg ggagagggt gaaaatgtcc 420
 gtccgtgtgt ggaatctttg ccagatggg cccctgcagg tacacgtctc tgcctgcca 480
 caccatgcct ggaagaacgc cttgtgtgtt gacatctgag gtagctgctt gtgtgttgcc 540
 gctctggagg ttggtagata cagaaccata ctgtccgta gccacgggat tgggtgtcct 600
 gatttctctt tcgtctgtaa tcatgacctt ttcaatgtcc acattagttt tcccagatc 660
 ttgttttcca aagatgagaa ccccgctctg aggaaaaaac ttttcttcat cgtccttgtg 720
 gctggccatg gccgggccc gattcaccag agagtctctt ccattaagggt ggtacttggt 780
 agctccagtc cacgagtatt cactgttgtt gttatccgca gatgtctttg atactcgtg 840

```

ctggcggtaa caggggtccag gaagccagtt cctagactgg tcccgaatgt cacttgctcc 900
ggcctgagaa aactgaagcc ttgactgcgt ggtggttccg cttggagtgt ttgttctgct 960
caagtaatac aggtactggt cgacgagagg attcatgaga cgggtccaaac tctggctgtg 1020
ggcgtagctg ctgtggaag gaacgtcttc aaagggtgtag ctgaaggtaa agttgtttcc 1080
ggtacgcagc atctgagaag gaaagtactc caggcagtaa aatgaagagc gtcctactgc 1140
ctgactcccg ttgttcaggg tgaggatccc atactgtggc accatgaaga cgtctgctgg 1200
gaacggcggg aggcacacct gatgcgccga gccgaggacg tacgggagct ggtactccga 1260
gtcagtaaac acctgaaccg tgcgtgtaag gttattggca atcgtcgtcg taccgtcatt 1320
ctgcgtgacc tccttgactt gaattgtaaa gagcttgaag ttgagtcttt tgggcccggg 1380
tcccccaattg ttgttgatga gtctttgccg gtcacgtggc gaaaagtggc agtggaatct 1440
gttgaaagta aaataccccc aaggggtgct gtagccaaag tagtggttgt cgtttgaggc 1500
tcctgattgg ctggaaatct gcctgtagag gtggttgttg taggtgggca gagcccaggt 1560
gcgggtgctg gtggtgatga ctctgtcgcc catccatgtg gaatcgcaat gccaatcttc 1620
cgaggaatta cccactccgt cggcgccctc gttattgtct gccattggtg cggcactgcc 1680
ttagaccatc gtattagttc ccagaccaga gggggctgct ggtggctgtc cgagaggctg 1740
ggggctcagg acggagtctg cgtctccagt ctgaccgaaa ttcaatctcc ttcttgagg 1800
ctgctggccc gcttttccgg ttcccaggga ggagtctggc tccgcaagag agtgctctac 1860
cggcctcttt ttcccggag ccgtcttaac aggttctca accaggccca gaggttcaag 1920
aaccctcttt ttgcctgga agactgctcg tccgaggttg ccccaaaaag acgtatcttc 1980
tttaagacgc tcctggaact ccgcgtcggc gtggtgtgac ttgaggtacg ggtgtctcc 2040
gccgtcagc tgccggtcgt aggccttgct gtgctcagg gccgcggcgt ctgcctcgtt 2100
gaccggctct ccctgtcga gtccgttgaa gggccaagg tacttgacc caggaagcac 2160
aagacccctg ctgctgctct tatgccgctc tgcgggcttt ggtggtggtg ggccagggtt 2220
gagcttcac cactgtctta ttcttcaga gagagtgtcc tcgagccaat ctggaagata 2280
accatcgga gccatactg atttaaatca ttattgttc agagatgcag tcatccaaat 2340
ccacattgac cagatcgcaa gcagtgaag cgtctggcac ctttcccatg atatgatgaa 2400
ttagcacag ttctgtatc gcctttttga cgacagaaac gggttgagat tctgacacgg 2460
gaaagcactc taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca 2520
ttctctcgca ttgtctgag ggaacagca tcagattcat gccacgtga cgagaacatt 2580
tgttttggt cctgtccgc tagttgattg aagcttccgc gtctgacgtc gatggctgcg 2640
caactgactc gcgcgccgt ttgggtcac ttatatctgc gtcactgggg gcgggtcttt 2700
ttttggctcc accctttttg acgtagaatt catgctctac ctcaaccacg tgatcctttg 2760
cccaccgaa aaagtctttg acttcctgct tggtagacct cccaaagtca tgatccagac 2820
ggcgggtgag ttcaaatgt aacatccggt cttgcaacgg ctgctggtgt tcgaaggctc 2880
ttgagttccc gtcaatcact gcgcacatgt tgggttgga ggtgacaatc acgggagtcg 2940
ggtctatctg ggcgaggac ttgcatctt ggtccacgcg caccttgctt cctccgagaa 3000
tggtttggc cgactccacg accttggcgg tcatcttccc ctctccac cagatcacca 3060
tctgtcgac gcaatcattg aaaggaaagt tctcattggt ccagttgacg cagcaagggc 3120
gaattcgttt aaacctgcag gactagctcc ttagtgagg g 3161

```

<210> 173
 <211> 3172
 <212> DNA
 <213> new AAV serotype, clone hu 173.4

```

<400> 173
gattgaattt agcggccgcg aattcgccct. tgcgtcgtca actggaccaa tgagaacttt 60
cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgaccgcc 120
aaggctcgtg agtccgccaa ggccattctg ggtggaagca aggtgcgcgt ggacccaaaag 180

```

tgcaagtcac	tgcccagat	cgacccacg	cccgtgatcg	tcacctcaa	caccaacatg	240
tcgcccgtga	tcgacgggaa	cagcaccacc	ttcgagcacc	agcagcccct	gcaggaccgc	300
atgttcaagt	tcgagctcac	ccgccgtctg	gagcacgact	ttggcaagg	gaccaagcag	360
gaagtcaaag	agttcttccg	ctgggctcag	gatcacgtga	ctgagggtggc	gcatgagtcc	420
tacgtcagaa	agggcggagc	caccaaaga	cccgcacca	gtgacgcgga	tataagcgag	480
cccaagcggg	cctgcccctc	agttgcggag	ccatcgacgt	cagacgcgga	agcaccggtg	540
gactttgcgg	acaggtacca	aaacaaatgt	tctcgtcacg	cgggcatgct	tcagatgctg	600
tttccttgca	agacatgcga	gagaatgaat	cagaatttca	acgtctgctt	cacgcacggg	660
gtcagagact	gctcagagt	cttccccggc	gcgtcggaat	ctcaaccctg	cgtcagaaaa	720
aagacgtatc	agaaactgtg	cgcgattcat	catctgctgg	ggcgggcacc	cgagattgctg	780
tgttcggcct	gcgatctcgt	caacgtggac	ttggatgact	gtgtttctga	gcaataaatg	840
acttaaacca	ggtatggctg	ctgacgggta	tcttcagat	tggtctgagg	acaacctctc	900
tgagggcatt	cgcgagtgg	gggacctgaa	acctggagcc	cccaagccca	aggccaacca	960
gcagaagcag	gacgacggcc	ggggctctgg	gcttcctggc	tacaagtacc	tcggaccctt	1020
caacggactc	gacaaggggg	agcccgtcaa	cgcgggcgac	gcagcggccc	tcgagcacga	1080
caaggcctac	gaccagcagc	tcaaagcggg	tgacaatccg	tacctgcggt	ataaccacgc	1140
cgacgccgag	tttcaggagc	gtctgcaaga	agatacgtct	tttgggggca	acctcgggctg	1200
agcagctctc	caggccaaga	agcgggttct	cgaacctctc	ggtctggttg	aggaagctgc	1260
taagacggct	cctggaaaaga	agagaccggt	agaaccgtca	cctcagcgtt	cccccgactc	1320
ctccgcgggc	atcggcaaga	aaggccagca	gcccgtctaa	aagagactga	actttggtca	1380
gactggcgac	tcagagtcag	tccccgaccc	tcaaccaatc	ggagaaccac	cagcaggccc	1440
ctctggtctg	ggatctggta	caatggctgc	aggcgggtggc	gctccaatgg	cagacaataa	1500
cgaaggcgcc	gacggagtgg	gtagttcctc	aggaaattgg	cattgcgatt	ccacatggct	1560
gggcgacaga	gtcatcacca	ccagcaccgc	aacctggggc	ctgcccacct	acaacaacca	1620
cctctacaag	caaatatcca	atgggacatc	gggaggaagc	accaacgaca	acacctactt	1680
cggctacagc	accccctggg	ggtattttga	cttcaacaga	ttccactgcc	acttctcacc	1740
acgtgactgg	cagcgactca	tcaacaacaa	ctggggattc	cggccaaaaa	gactcagctt	1800
caagctcttc	aacatccagg	tcaaggaggt	cacgcagaat	gaaggcaccg	agaccatcgc	1860
caataacctt	accagcacga	ttcagggtatt	tacggactcg	gaataaccagc	tgccgtacgt	1920
cctcggctcc	gcgcaccagg	gctgcctgcc	tccgttccc	gcggacgtct	tcattgattcc	1980
ccagtacggc	taccttacac	tgaacaatgg	aagtcaagcc	gtaggccgtt	cctccttcta	2040
ctgcctggaa	tattttccat	ctcaaagtct	gcgaactgga	aacaattttg	aattcagcta	2100
caccttcgag	gacgtgcctt	tccacagcag	ctgcgcacac	agccagagct	cggaccgact	2160
gatgaatcct	ctcatcgacc	agtacctgta	ctacttatcc	agaactcgg	ccacaggagg	2220
aactcaagg	acccagcaat	tgttattttc	tcaagctggg	cctgcaaaca	tgctgggtca	2280
ggctaagaac	tggtctacctg	gaccttgcta	ccggcagcag	cgagtctcta	cgacactgtc	2340
gcaaaacaac	aacagcaact	ttgcttggac	tggtgccacc	aaatatcacc	tgaacggaag	2400
agactctttg	gtaaatcccc	gtgtcgccat	ggcaaccac	aaggacgacg	aggaacgctt	2460
cttcccgtcg	agtggagtcc	tgatgtttgg	aaaacagggt	gctggaagag	acaatgtgga	2520
ctacagcagc	gttatgctaa	ccagcgaaga	agaaattaaa	accactaacc	ctgtagccac	2580
agaacaatac	ggtgtgtgtg	ctgacaactt	gcagcaaac	aatacagggc	ctattgtggg	2640
aatgtcaac	agccaaggag	ccttacctgg	catggtctgg	cagaaccgag	acgtgtacct	2700
gcagggtccc	atctgggcca	agattcctca	cacggacggc	aacttcacc	cttcaccgct	2760
aatgggagga	tttggactga	agcaccaccc	tcctcagatc	ctgatcaaga	acacgccggt	2820
acctgcggat	cctccaacaa	cgttcagcca	ggcgaaattg	gcttccttca	ttacgcagta	2880
cagcaccgga	cagggtcagc	tggaatcga	gtgggagctg	cagaaggaga	acagcaaacg	2940

ctggaaccca gagattcagt acatttcaaa ctactacaaa tctacaaatg tggactttgc	3000
tgtcaatata gaggggaactt attctgagcc tcgccccatt ggtactcgtt acctcaccgc	3060
taatctgtaa ttgctgggta atcaataaac cgtttgattc gtttcagttg aactttggtc	3120
tctgcgaagg gcgaattcgt ttaaaccctgc aggactagtc ccttttagtga gg	3172

<210> 174
 <211> 3159
 <212> DNA
 <213> new AAV serotype, clone hu 161.8

<400> 174	
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt	60
cctttcaatg attgctgcga caagatgggtg atctgggtggg aggagggaaa gatgaccgcc	120
aaggctcgtg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa	180
tgcaagtctt cgcccagat agaccgcact cccgtgattg tcacctcaa caccgacatg	240
tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg	300
atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggc caccaagcag	360
gaagtcaaa actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc	420
tacgtcaaaa aggggtggagc taagaaaaga cccgccccca gtgacgcaga tataagttag	480
cccaaaccgg cgcgcgagtc agttgcgcag ccacgcacgt cagacgcgga agcttcgatc	540
aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg	600
tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga	660
cagaaagact gtttagagtg ctttcccgtg tcagaatctc aaccggttgc tgctgtcaaa	720
aaggcgtatc agaaactttg ctacattcat catatcatgg gaaagggtgcc agacgcttgc	780
actgcctgcg atctgggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt	840
taaatacagg atggctgccc atgggttatct tccagattgg ctcgaggaca ctctctctga	900
aggaataaga cagtgggtgga agctcaaaac tggcccacca ccaccaaagc ccgcagagcg	960
gcataaggac gacagcaggg gtctttgtgct tcctgggtac aagtacctcg gacccttcaa	1020
cggactcgac aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa	1080
ggcctacgac cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga	1140
cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc	1200
agtcttccag gcaaaaaaga ggggttctga acctctgggc ctgggttagg aacctgttaa	1260
aacggctccg ggaaaaaaga ggccggtaga gcacctctct gtggagccag actcctcctc	1320
gggaaccgga aaagcgggac agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg	1380
agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctg	1440
tctgggatct actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg	1500
tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga	1560
cagagtcac accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta	1620
caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac	1680
cccctggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca	1740
aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa	1800
cattcaagtc aaagagggtc cgcagaatga cggtagcagc acgattgccg ataaccttac	1860
cagcacgggt cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc	1920
gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atgggtccac agtatggata	1980
cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta	2040
ctttccttct cagatgctgc gtaccggaaa caactttcag ttcagctaca cttttgaaga	2100
cgtgccttct cacagcagct acgctcacag ccagagtctg gatcgggtga tgaatcctct	2160
gatcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca	2220
gtctcggcta ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaaccg	2280

```

gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa 2340
cagcaacttt ccctggaccg cagctacaaa gtatcatcta aatggccggg actcgttggg 2400
taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtgtt tccccatgca 2460
tggaaccctt atatttggtg aacaaggaa aaatgccaac gacgcggatt tggaaaatgt 2520
catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg 2580
aactgtatca aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatca 2640
ccaaggagcg ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat 2700
ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactgg tgggagggtt 2760
tggactcaaa caccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc 2820
tcccacaaac ttcagtctcg ccaagtttgc ttctttcatc acacagtatt ccacggggca 2880
ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga 2940
aattcagtag acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa 3000
tgggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060
gcttggttaat caataaacg ttttaattcgt ttcagttgaa ctttggcttc tgcgaagggc 3120
gaattcggtt aaacctgcag gactagtccc ttagtgag 3159

```

```

<210> 175
<211> 3172
<212> DNA
<213> new AAV serotype, clone hu 173.8

```

```

<400> 175
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60
cccttcaacg attgctcgca caagatgggtg atctgggtggg agggaggcaa gatgaccgcc 120
aaggctcgtg agtccgccaa ggccattctg ggtggaagca aggtgcgcgt ggaccaaag 180
tgcaagtcac cggcccagat cgacccacg cccgtgatcg tcacctcaa caccaacatg 240
tgcgccgtga tcggcgggaa cagcaccacc ttcgagcacc agcagccctt gcaggaccgc 300
atgttcaagt tcgagctcac ccgctgtctg gagcacgact ttggcaaggt gaccaagcag 360
gaagtcaaag agttcttccg ctgggctcag gatcacgtga ctgaggtggc gcatgagttc 420
tacgtcagaa agggcggagc caccaaaaga cccgccccca gtgacgcgga tataagcgag 480
cccaagcggg cctgccccctc agttgcggag ccatcgacgt cagacgcgga agcaccggtg 540
gactttgcgg acaggtagca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg 600
tttccctgca agacatgcga gagaatgaat cagaatttca acgtctgctt cagcacggg 660
gtcagagact gctcagagtg cctccccggc gcgtcagaat ctcaaccctg cgtcagaaaa 720
aagacgtatc agaaactgtg cgcgattcat catctgttgg ggcgggcacc cgagattgctg 780
tggttcggct gcgatctcgt caacgtggac ttggatgact gtgtttctga gcaataaatg 840
acttaacca ggtatggctg ctgacgggta tcttcagat tggctcgagg acaacctctc 900
tgagggcatt cgcgagtggg gggacctgaa acctggagcc cccaagccca aggccaaacca 960
gcagaagcag gacgacggcc ggggtctggg gcttcttggc tacaagtacc tcggaccctt 1020
caacggactc gacaaggggg agcccgtcaa tgcggcggac gcagcggccc tcgagcacga 1080
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggg ataaccacgc 1140
cgacgccgag tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg 1200
agcagtcttc caggccaaga agcgggttct cgaacctctc ggtctggttg aggaagctgc 1260
taagacggct cctggaaaga agagaccggg agaaccgtca cctcagcgtt cccccgactc 1320
ctccacgggc atcggcaaga aaggccagca gcccgctaaa aagagactga actttgggtca 1380
gactggcgac tcagagtcag tccccgacct tcaaccaatc ggagaaccac cagcaggccc 1440
ctctgggtct ggatctggta caatggctgc aggcgggtgg gctccaatgg cagacaataa 1500
cgaaggcgcc gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct 1560
gggcgacaga gtcacacca ccagcaccgg aacctggggc ctgccacct acaacaacca 1620

```


cctctacaag caaatatcca atgggacatc gggaggaagc accaacgaca acacctactt 1680
 cggctacagc accccctggg ggtatattga cttcaacaga ttccactgcc acttctcacc 1740
 acgtgactgg cagcgactca tcaacaacaa ctggggattc cggccaaaaa gactcagctt 1800
 caagctcttc aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc 1860
 caataacctt accagcacga ttcagggtatt tacggactcg gaataccagc tgccgtacgt 1920
 cctcggctcc gcgcaccagg gctgcctgcc tccgttcccc gcggacgtct tcatgattcc 1980
 ccagtacggc taccttacac tgaacaatgg aagtcaagcc gtaggccgtt cctccttcta 2040
 ctgcctggaa tattttccat ctcaaagtct gcgaactgga aacaattttg aattcagcta 2100
 caccttcgag gacgtgcctt tccacagcgg ctacgcacac agccagagct tggaccgact 2160
 gatgaatcct ctcatcgacc agtacctgta ctacttatcc agaactcagt ccacaggagg 2220
 aactcaaggt acccgacaat tggtattttc tcaagctggg cctgcaaaca tgtcggctca 2280
 ggctaagaac tggctacctg gaccttgcta ccggcagcag cgagtctcta cgacactgtc 2340
 gcaaaaac aacagcaact ttgcttggaac tgggtgccacc aaatatcacc tgaacggaag 2400
 agactctttg gtaaatcccc gtgtcgccat ggcaaccac aaggacgacg aggaacgctt 2460
 cttcccgtcg agtggagtcc tgatgtttgg aaaacagggg gctggaagag acaatgtgga 2520
 ctacagcagc gttatgctaa ccagcgaaga agaaattaaa accactaacc ctgtagccac 2580
 agaacaatac ggtgtggtgg ctgacaactt gcagcaaacc aatacagggc ctattgtggg 2640
 aaatgtcaac agccaaggag ccttacctgg catggtctgg cagaaccgag acgtgtacct 2700
 gcagggtccc atctgggcca agattcctca cacggacggc aacttccacc cttaccgct 2760
 aatgggagga tttggactga agcaccacc tcctcagatc ctgatcaaga acacgccggt 2820
 acctgcggat cctccaacga cgttcagcca ggcgaattg gcttccttca ttacgcagta 2880
 cagcaccgga caggtcagcg tggaaatcga gtgggagctg cagaaggaga acagcaaacg 2940
 ctggaacca gagattcagt acacttcaaa ctactacaaa tctacaaatg tggactttgc 3000
 tgtcaataca gagggaactt attctgagcc tcgccccatt ggtactcgtt acctcaccg 3060
 taatctgtaa ttgctggtta atcaataaac cgtttgattc gtttcagttg aactttggctc 3120
 tctgcgaagg gcgaattcgt ttaaacctgc aggactagtc cctttagtga gg 3172

<210> 176

<211> 3160

<212> DNA

<213> new AAV serotype, clone hu 145.1

<400> 176

acccttcaact aaagggacta gtcctgcagg tttaaagcaa ttcgcccttg ctgcgtcaac 60
 tggaccaatg agaactttcc cttcaacgac tgtgtcgaca agatgggtgat ttggtgggag 120
 gaggggaaga tgaccgcaa ggtcgtggag tcggccaaag ccattctcgg aggaagcaag 180
 gtgcgcgtgg accagaaatg caagtcctcg gccagatag atccgactcc cgtgatcgtc 240
 acctccaaca ccaacatgtg cgccgtgatt gacgggaact caacgacctt cgaacaccag 300
 cagccgttgc aagaccggat gttcaaattt gaactcacc gccgtctgga tcatgacttt 360
 ggggaaggta ccaagcggga agtcaaagac tttttccggt gggcaaagga tcacgtgggt 420
 gaggtggagc atgaattcta cgtcaaaaag ggtggagcca agaaaagacc cgcccctagt 480
 gacgcagata taagttagcc caaacgggtg cgcgagtcag ttgcgcagcc atcgacgtca 540
 gacgcggaag cttcgatcaa ctacgcggac aggtaccaaa acaaatgttc tcgtcacgtg 600
 ggcataatc tgatgctgtt tccctgcaga caatgcgaga gaatgaatca aaattcaaat 660
 atctgcttca ctcacggaca gaaagactgt ttagagtgtc ttcccgtgtc agaattctca 720
 cctgtttctg tcgtcaaaaa ggcgtatcag aaactgtgct acattcatca tatcatggga 780
 aagggtccag acgcttgac tgccctgcgat ctggtcaatg tggatttggga tgactgcac 840
 tctgaacaat aaatgattta aatcaggat ggtgcggat ggttatcttc cagattggct 900
 cgaggacact ctctctgaag gaataagaca gtggtggaag ctcaaacctg gccaccacc 960

accaaagccc gcagagcggc ataaggacga cagcaggggt cttgtgcttc ctgggtacaa 1020
 gtacctcgga cccctcaacg gactcgacaa gggagagccg gtcaacgagg cagacgccgc 1080
 ggccctcgag cagacaagg cctacgaccg gcagctcgac agcggagaca acccgtaacct 1140
 caagtacaac cagcccgacg cggagtttca ggagcgtctt aaagaagata cgtcttttgg 1200
 gggcaacctc ggacgagcag tcttccaggc gaaaaagagg gttcttgaac ctctgggcct 1260
 ggttgaggaa cctgttaaga cggctccggg aaaaaagagg ccggtagagc actctcctgc 1320
 ggagccagac tcctcctcgg gaaccggaaa agcgggccag cagcctgcaa gaaaaagact 1380
 gaatttcggt cagactggag acgcagactc cgtacctgac cccagacctc tcagacagcc 1440
 accagcagcc cccacaagtt tgggatctac tacaatggct acaggcagtg gcgcaccaat 1500
 ggcagacaat aacgaggggt cggatggagt gggtaattcc tcaggaaatt ggcattgcca 1560
 ttcccaatgg ctgggcgaca gagtcatcac caccagcacc cgaacctggg ccctgcccac 1620
 ctacaacaac cacttttaca agcaaatctc cagccaatca ggagcctcaa acgacaacca 1680
 ctactttggc tacagcacc cctgggggta ttttgacttc aacagattcc actgccactt 1740
 ttcaccacgt gactggcaaa gactcatcaa caacaactgg ggattccgac ccaagagact 1800
 caacttcaag ctctttaaca ttcaagtcaa agaggtcacg cagaatgacg gtacgacgac 1860
 gattgccaat aaccttacca gcacggttca ggtgtttact gactcggagt accagctccc 1920
 gtacgtcctc ggctcggcgc atcaaggatg cctcccgcg tttccagcgg acgtcttcat 1980
 ggtcccacag tatggatacc tcacctgaa caacgggagt caggcggtag gacgtcttc 2040
 cttttactgc ctggagtact ttccttctca gatgtctcgt actggaaaca actttcagtt 2100
 cagctacact tttgaagacg tgcctttcca cagcagctac gctcacagcc agagtttgga 2160
 tcggctgatg aatcctctga tcgaccagta cctgtattat ctaaacagaa cacaacagc 2220
 tagtggaaact cagcagcttc ggctactgtt tagccaagct ggaccacaa gcatgtctct 2280
 tcaagctaaa aactggctgc ctggaccgtg ttatcgccag cagcgtttgt caaagcaggc 2340
 aaacgacaac aacaacagca actttccctg gactggagct accaagtact acctcaatgg 2400
 cagagactct ttgtgaacc cgggcccggc catggccagc cacaaggacg atgaagaaaa 2460
 gtttttcccc atgcatggaa ccctaattatt tggtaaagaa ggaacaaatg ctaccaacgc 2520
 ggaattggaa aatgtcatga ttacagatga agaggaaatc aggaccacca atcccgtggc 2580
 tacagagcag tacggatatg tgtcaaataa tttgcaaac tcaaatactg ctgcaagtac 2640
 tgaaactgtg aatcaccaag gagcattacc tggatgggtg tggcaggatc gagacgtgta 2700
 cctgcaggga cccatttggg ccaagattcc tcacaccgat ggacacttcc atccttctcc 2760
 actgatggga ggttttggac tcaaacaccc gcctcctcag attatgatca aaaacactcc 2820
 cgttccagcc aatcctcca caaacttcag ttctgccaag tttgcttctc tcatcacaca 2880
 gtattccacg ggacaggtca gcgtggagat cgagtgggag ctgcagaagg agaacagcaa 2940
 acgctggaat cccgaaattc agtacacttc caactacaac aaatctgtta atgtggactt 3000
 tactgtggac actaatggtg tgtattcaga gcctcgcccc attggcacca gatacctgac 3060
 tcgtaatctg taattgcttg ttaatcaata aaccgtttaa ttcgtttcag ttgaactttg 3120
 gtctctgcga agggcgaatt cgcggccgct aaatcaatcg 3160

<210> 177
 <211> 3157
 <212> DNA
 <213> new AAV serotype, clone hu 145.5

<400> 177
 ctactaagg gactagtcct gcaggtttaa acgaattcgc ccttgctgcg tcaactggac 60
 caatgagaac tttcccttca acgactgtgt cgacaagatg gtgatttggg gggaggaggg 120
 gaagatgacc gccaaaggctg tggagtcggc caaagccact ctcgaggaa gcaagggtgcg 180
 cgtggaccag aaacgcaagt cctcggccca gatagatccg actcccgta tcgtcacctc 240
 caacaccaac atgtgcgccc tgattgacgg gaactcaacg accttcgaac accagcagcc 300

gttgcaagac cgaatgttca aatttgaact caccgcgcgt ctggatcatg acttcgggaa	360
ggtcaccaag caggaagtca aagacttttt ccggtgggca aaggatcacg tggttgaggt	420
ggagcatgaa ttctacgtca aaaaggggtg agccaagaaa agacccgccc ctagtgacgc	480
agatataagt gagcccaaac ggggtgcgca gtcagttgcg cagccatcga cgtcagacgc	540
ggaagcttcg atcaactacg cggacaggta ccaaaacaaa tggttctcgtc acgtgggcat	600
gaatctgatg ctgtttccct gcagacaatg cgagagaatg aatcaaaatt caaatatctg	660
cttcaactcac ggacagaaag actgtttaga gtgtttccc gtgtcagaat ctcaacctgt	720
ttctgtcgtc aaaaaggcgt atcagaaact gtgtacatt catcatatca tgggaaagggt	780
gccagacgct tgcactgcct gcgatctggt caatgtggat ttggatgact gcattctctga	840
acaataaatg atttaaatca ggtatggctg ccgatggtta tcttcagat tggctcgagg	900
acactctctc tgaaggaata agacagtggg ggaagctcaa acctggccca ccaccacaa	960
agcccgacga gcggcataag gacgacagca ggggtcttgt gcttcctggg tacaagtacc	1020
tcggaccctt caacggactc gacaagggag agccgggtcaa cgaggcagac gccgcggctc	1080
tcgagcacga caaggcctac gaccggcagc tcgacagcgg agacaacccg tacctcaagt	1140
acaaccacgc cgacgcggag ttctcaggag gtcttaaaga agatacgtct tttgggggca	1200
acctcggacg agcagctctc caggcgaaaa agaggggtct tgaacctctg ggcctggtg	1260
aggaacctgt taagacggct ccgggaaaaa agaggccggt agagcactct cctgcggagc	1320
cagactcttc ctcgggaacc ggaaaagcgg gccagcagcc tgcaagaaaa agactgaatt	1380
tcggtcagac tggagacgca gactccgtac ctgaccccca gcctctcgga cagccaccag	1440
cagccccac aagtttggga tctactacaa tggctacagg cagtggcgca ccaatggcag	1500
acaataacga ggggtgccat ggagtgggta attcctcagg aaattggcat tgcgattccc	1560
aatggctggg cgacagagtc atcaccacca gcaccggaac ctggggccctg cccacctaca	1620
acaaccacct ttacaagcaa atctccagcc aatcaggagc ctcaaacgac aaccactact	1680
ttggctacag caccctctg gggatatttg acttcaacag attccactgc cgcttttcac	1740
cacgtgactg gcaaagactc atcaacaaca actggggatt ccgacccaag agactcaact	1800
tcaagctctt taacattcaa gtcaaagagg tcacgcagaa tgacggtagc acgacgattg	1860
ccaataacct taccagcacg gttcagggtt ttactgactc ggagtaccag ctcccgtacg	1920
tcctcggctc ggcgcatcaa ggatgcctcc cgccgtttcc agcggacgct ttcattggtcc	1980
cacagtatgg atacctcacc ctgaacaacg ggagtacggc ggtaggacgc tcttcctttt	2040
actgcctgga gtactttcct tctcagatgc tgcgtactgg aaacaacttt cagttcagct	2100
acacttttga agacgtgcct ttccacagca gctacgctca cagccagggt ttggatcggc	2160
tgatgaatcc tctgatcgac cagtacctgt attatctaaa cagaacacaa acagctagtg	2220
gaactcagca gtctcggcta ctgtttagcc aagctggacc cacaagcatg tctcttcaag	2280
ctaaaaactg gctgcctgga ccgtgttatc gccagcagcg tttgtcaaag caggcaaacg	2340
acaacaacaa cagcaacttt ccctggactg gagctaccaa gtaccacctc aatggcggag	2400
actctttggt gaacccgggc ccggccatgg ccagccacaa ggacgatgaa gaaaagtgtt	2460
tccccatgca tggaaacctc atatttggta aagaaggaa aaatgtacc aacgcggaat	2520
tggaaaatgt catgattaca gatgaagagg aaatcaggac caccaatccc gtggctacag	2580
agcagtacgg atatgtgtca aataatttgc aaaactcaaa tactgctgca agtactgaaa	2640
ctgtgaatca ccaaggagca ttacctggtg tgggtgtggc ggatcgagac gtgtacctgc	2700
ggggacccat ttgggccaag attcctcacg ccgatggaca ctttcacct tctccactga	2760
tgggaggttt tggactcaaa caccgcctc ctcagattat gatcaaaaac actcccgttc	2820
cagccaatcc tcccacaac ttcagttctg ccaagtttgc ttccttcac acacagtatt	2880
ccacgggaca ggtcagcgtg gagatcaggt gggagctgca gaaggagaac agcaaacgct	2940
ggaatcccga aattcagtac acttccaact acaacaatc tgtaaatgtg gactttactg	3000

tgggacactaa tgggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta 3060
 atctgtaatt gcttgtaaat caataaaccg ttaattcgt ttcagttgaa ctttggcttc 3120
 tgcgaagggc gaattcgcgg ccgctaaatt caattcg 3157

 <210> 178
 <211> 3163
 <212> DNA
 <213> new AAV serotype, clone hu 145.6

 <400> 178
 accctcacta aagggactag tcctgcaggt ttaaacgaat tcgcccttgc tgcgtcaact 60
 ggagcaatga gaactttccc ttcaacgact gtgtcgacaa gatggtgatt tgggtggagg 120
 aggggaagat gaccgccaag gtcgtggagt cgcccaaagc cattctcga ggaagcaagg 180
 tgcgcgtgga ccagaaatgc aagtccctcg cccagataga tccgactccc gtgatcgtca 240
 cctccaacac caacatgtgc gccgtgattg acgggaactc aacgacctc gaacaccagc 300
 agccgttgca agaccggatg ttcaaatttg aactcaccg ccgtctggat catgactttg 360
 ggaaggctac caagcaggaa gtcaaagact ttttccggtg ggcaaaggat cacgtggttg 420
 aggtggagca tggattctac gtcaaaaagg gtggagccaa gaaaagaccc gcccttagtg 480
 acgcagatat aagttagccc aaacgggtgc gcgagtcagt tgcgcagcca tcgacgtcgg 540
 acgcggaagc ttcgatcaac tacgcggaca ggtacaaaa caaatgttct cgtcacgtgg 600
 gcatgaatct gatgctgttt ccctgcagac aatgcgagag aatgaatcaa aattcaaata 660
 tctgcttcac tcacggacag aaagactgtt tagagtgtt tcccgtgtca gaatctaac 720
 ctgtttctgt cgtcaaaaag gcgtatcaga aactgcgcta cattcatcat atcatgggaa 780
 aggtgccaga cgcttgcaat gcctgcgac tggtcaatgt ggatttggat gactgcatct 840
 ctgaacaata aatgatttaa atcaggatag gctgccgatg gttatcttcc agattggctc 900
 gaggacactc tctctgaagg aataagacag tgggtgaagc tcaaacctgg cccaccacca 960
 ccaaagcccc cagagcggca taaggacgac agcaggggtc ttgtgcttcc tgggtacaag 1020
 tacctcggac ctttaacgg actcgacaag ggagagccgg tcaacgaggc agacgccgcg 1080
 gccctcagac acgacaaggc ctacgaccgg cagctcgaca gcggagacaa cccgtacctc 1140
 aagtacaacc acgccgacgc ggagtttcag gagcgtctta aagaagatac gtcttttggg 1200
 ggcaacctcg gacgagcagt cttccaggcg aaaaagaggg ttcttgaacc tctgggcctg 1260
 gttgaggaac ctgttaagac ggctccggga aaaaagaggc cggtagagca ctctcctgcg 1320
 gagccagact cctcctcggg aaccggaaaa gcgggcccagc agcctgcaag aaaaagactg 1380
 aatttcggtc agactggaga cgcagactcc gtacctgacc cccagcctct cggacagcca 1440
 ccagcagccc ccacaagttt gggatctact acaatggcta caggcagtgg cgcaccaatg 1500
 gcagacaata acgagggtgc cgatggagtg ggtaattcct caggaaattg gcattgcgat 1560
 tcccaatggc tgggcgacag agtcatcacc accagcacc gaacctgggc cctgcccacc 1620
 tacaacaacc acctttacaa gcaaatctcc agccaatcag gagcctcaa gcacaaccac 1680
 tactttggct acagcacccc ctgggggtat tttgacttca acagattcca ctgccacttt 1740
 tcaccacgtg actggcaaa actcatcaac aacaactggg gattccgacc caagagactc 1800
 aacttcaagc tctttaacat tcaagtcaaa gaggtcacgc agaattgacg tacgacgacg 1860
 attgccaata accttaccag cacggttcag gtgtttactg actcggagta ccagctcccg 1920
 tacgtcctcg gctcggcgca tcaaggatgc ctcccgcgt tccagcggga cgtcttcatg 1980
 gtccacagat atggatacct caccctgaac aacgggagtc aggcggtagg acgctcttcc 2040
 ttttactgcc tggagtgtt tcttctcag atgtgcgta ctggaaacaa ctttcagttc 2100
 agctacactt ttgaagacgt gcctttccac agcagctacg ctacagcca gagtttggat 2160
 cggctgatga atcctctgat cgaccagtac ctgtattatc taaacagaac acaaacagct 2220
 agtggaaactc agcagctctg gctactgttt agccaagctg gaccacaag catgtctctt 2280
 caagctaaaa actggctgcc tggaccgtgt tatcgccagc agcgtttgtc aaagcaggca 2340

```

aacgacaaca acaacagcaa ctttccttgg actggagcta ccaagtacca cctcaatggc 2400
agagactctt tggatgaacc gggcccgcc atggccagcc acaaggacga tgaagaaaag 2460
tttttcccca tgcattgaac cctaataatt ggtaaagaag gaacaaatgc taccaacgcg 2520
gaattggaaa atgtcatgat tacagatgaa gaggaatca ggaccaccaa tcccgtggct 2580
acagagcagt acggatatgt gtcaaataat ttgcaaaact caaatactgc tgcaagtact 2640
gaaactgtga atcaccaagg agcattacct ggtatggtgt ggcaggatcg agacgtgtac 2700
ctgcagggac ccatttgggc caagattcct cacaccgatg gacactttca tccttctcca 2760
ctgatgggag gttttggact caaacaccg cctcctcaga ttatgatcaa aaacactccc 2820
gttccagcca atcctcccac aaacttcagt tctgccaagt ttgcttctt catcacacag 2880
tattccacgg gacaggtcag cgtggagatc gagtgggagc tgcagaagga gaacagcaaa 2940
cgctggaatc ccgaaattca gtacacttcc aactacaaca aatctgttaa tgtggacttt 3000
actgtggaca ctaatggtgt gtattcagag cctcgcccca ttggcaccag atacctgact 3060
cgtaaatctgt aattgcttgt taatcaataa accgtttaat tcgtttcagt tgaactttgg 3120
tctctgcgaa gggcgaattc gcggccgcta aattcaattc gcc 3163

```

```

<210> 179
<211> 3161
<212> DNA
<213> new AAV serotype, clone hu 156.1

```

```

<400> 179
cgaattgatt tagcggccgc gaattcgccc ttcgcagaga ccaaagttca actgaaacga 60
attaaacggt ttattgatta acaagcaatt acagattacg agtcaggat ctggtgccaa 120
tggggcgagg ctctgaatac acaccattag tgtccacagt aaagtcacac ttaacagatt 180
tggtgtagtt ggaagtgtac tggatctcgg gattccagcg ttgctgttc tccttctgta 240
gtctccactc gatctccacg ctgaccgccc ccgtggaata ctgtgtgatg aaggaagcaa 300
actttgccgc actgaagggt gtcgaaggat tcgcaggtag cggggtgttt ttgatgagaa 360
tctgtggagg aggggtgttta agtccgaatc cgcccatgag gggagagggg tgaaaatgtc 420
cgctccgtgt cggaatcttt gccagatag gcccctgcag gtacacgtct ctgtcctgcc 480
agaccatgcc tggagaagac ccttgtgtgt tgacatctgc agtagatgct tgtgtgttgc 540
cgctctggag gttggtgatg acagaacat actgctccgt ggcacggga ttggtggttc 600
tgatttctc tcgtctgta atcatgacct ttccaatgtc cacatttgtt ttctctgatc 660
cttgttttcc aaagatgaga acccgcctct gaggaaaaaa ctttcttca tcgtccttgt 720
ggctggccat tgccgggccc ggattcacca gagagtctct gccattgagg tggactttgg 780
tagctccaat ccacgagtat tcaactgtgt tgtgtccgc agatgtcttt gatactcgct 840
gctggcggta acaggggtcca ggaagccagt tcctagactg atcccgaatg tcaactcgctc 900
cggcctgaga aaactgaagc ctggactgct tgggtgttcc gcttgagtg tttgttctgc 960
tcaagtaata caggtagtgg tcgatgagag gattcatgag acggtccaaa ctctggctgt 1020
gagcgtagct gctgtggaag ggaacatcct caaagggtga gctgaaggta aagttgtttc 1080
cggtagcgag catctgagaa gggaaagtact ccaggcagta aaatgaagag cgtcctactg 1140
cctgactccc gttgttcagg gtgaggatc catactgtgg caccatgaag acgtctgctg 1200
ggaaacggcg gaggcacctt tgatgcgccc agccgaggac gtacgggagc tggtagtccc 1260
agtcagttaa cacctgaacc gtgtgtgtaa ggattattggc aatcgtcgtc gtaccatcat 1320
tctgcgtgac ctctctgact tgaatgttaa agagcttgaa gttgagtctc ttgggccgga 1380
atccccagtt gttgttgatg agtctttgcc agtcacgtgg tgaaaagtgg cagtggaatc 1440
tgttgaaagc aaaatacccc caaggggtgc tgtagccaaa gtagtggttg tcgttgctgg 1500
ctctgtattg gctggaaatc tgctgtgaca gatggtgtgt gtaggtgggc agagcccagg 1560
ttcgggtgct ggtgtgtgat actctgtcgc ccacccatgt ggaatcgcaa tgccaatttc 1620
ccgaggaatt acccactccg tcggcgccat cgttattgtc tgccattggt gcgccactgc 1680

```

ctgttagccat cgtattagtt cccagaccag agggggctgc tgggtggctgt ccgagaggct 1740
 gggggtcagg tacggagctt gcgtctccag tctgaccgaa attcaatctc tttcttgag 1800
 gctggttgcc cgcttttccg gtccccgagg aggagttctg ctcacagga gagtgtctta 1860
 ccggcctctt ttttcccgga gccgtcttaa caggctcctc aaccaggccc agaggttcaa 1920
 gaaccctctt ttttgcctgg aagactgctc gtccgagggt gccccaaaa gacgtatctt 1980
 cttaaggcg ctctgaaac tccgcgtcgg cgtggctgta cttgaggtag gggttgtctc 2040
 cgctgtcgag ctgccggtcg taggccttgt cgtgtctgag ggccgcgcg tctgcctcgt 2100
 tgaccggctc tcccttgtcg agtccgtga agggtcgag gtacttgtag ccaggaagca 2160
 caagaccctt gctgtcgtcc ttatgccgct ctgcgggctt tgggtgggtt gggccagggt 2220
 tgagcttcca cactgtctt attccttcag agagagtgct ctcgagcaa tctggaagat 2280
 aaccatcggc agccatacct gatttaaattc atttattgtt cagagatgca gtcattcaaa 2340
 tccacattga ccagatcgca ggcagtgcaa gcgtctggca ctttcccat gatattgaga 2400
 atgtagcaaa gtttctgata cgctttttt acgacagaaa cgggttgaga ttctgacacg 2460
 ggaaagcact ctaaagcgtc tttctgtccg tgagtgaagc agatatttga attctgattc 2520
 attctctcgc attgtctgca gggaaacagc atcagattca tgcccacgtg acgagaacat 2580
 ttgttttggg acctgtccgc gtagttgac gaagcttccg cgtctgacgt cgatggctgc 2640
 gcaactgact cgcgcgccc tttgggtcct cttatatctg cgtcactggg ggcgggtctt 2700
 ttcttggtc caccctttt gacgtagaat tcatgtcca cctcaaccac gtgattcttt 2760
 gccaccgga aaaagctctt cacttcctgc ttggtgacct tcccaaagtc atgatccaga 2820
 cggcggttga gttcaaattt gaacatccgg tcttgcaacg gctgtgtgtg ttcgaaggtc 2880
 gttgagttcc cgtcaatcac ggcgcacatg ttggtgttgg aggtggcgat cacgggagtc 2940
 gggcttatct gggccgagga cttgcacttt tgggtccacg gcaccttgct tcctccgaga 3000
 atggcttcgg ccgattccac gaccttgcg gtcatctttc cctcctcca ccagatcacc 3060
 atcttgtcga cacagtcgtt gaagggaaag ttctcattgg tccagttgac gcagcaaggg 3120
 cgaattcgtt taaacctgca ggaactagtc ccttagtgag g 3161

<210> 180
 <211> 4721
 <212> DNA
 <213> adeno-associated virus serotype 7

<400> 180
 ttggccactc cctctatgcg cgctcgtcgt ctcgggtggg cctgcggacc aaagggtccgc 60
 agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcat agagggagtg 120
 gccaaactcca tctactagggg tacgcggaag cgctccac gctgccgcgt cagcgtgac 180
 gtaaatcacg tcatagggga gtggctcctgt attagctgtc acgtgagtgct ttttgcgaca 240
 ttttgcgaca ccacgtggcc atttgaggta tatatggccg agtgagcgag caggatctcc 300
 attttgaccg cgaaatttga acgagcagca gccatgccgg gtttctacga gatcgtgatc 360
 aagggtgccg gcgacctgga cgagcacctg ccgggcattt ctgactcgtt tgtgaactgg 420
 gtggccgaga aggaatggga gctgccccg gattctgaca tggatctgaa tctgatcgag 480
 caggcaccctc tgaccgtggc cgagaagctg cagcgcgact tcctggtcca atggcgccgc 540
 gtgagtaagg ccccgaggc cctgttcttt gttcagttcg agaagggcga gagctacttc 600
 caccttcacg ttctggtgga gaccacgggg gtcaagtcca tgggtgtagg ccgttctctg 660
 agtcagattc gggagaagct ggtccagacc atctaccgcg gggtcgagcc cacgctgccc 720
 aactggttcg cggtgacaa gacgcgtaat ggcgcggcg gggggaacaa ggtggtggac 780
 gagtgtaca tccccacta cctcctgccc aagaccagc ccgagctgca gtgggcgtgg 840
 actaacatgg aggagtatat aagcgcgtgt ttgaacctgg ccgaacgcaa acggtcctg 900
 gcgcagcacc tgaccacgt cagccagacg caggagcaga acaaggagaa tctgaacccc 960
 aattctgacg cggcgtgat cagggtcaaaa acctccgcgc gctacatgga gctggctcggg 1020

"tggtctggtgg accggggcat cactctccgag aagcagtgga tccaggagga ccaggcctcg 1080
 tacatctcct tcaacgccgc ctccaactcg cggctccaga tcaaggccgc gctggacaat 1140
 gccggcaaga tcatggcgct gaccaaattc gcgcccact acctgggtggg gccctcgctg 1200
 cccgaggaca ttaaaaccaa ccgcatctac cgcatcctgg agctgaacgg gtacgatcct 1260
 gcctacgccg gctccgtctt tctcggctgg gccagaaaa agttcgggaa gcgcaacacc 1320
 atctggctgt ttgggcccgc caccaccggc aagaccaaca ttgcggaagc catcgccac 1380
 gccgtgcctt tctacggctg cgtcaactgg accaatgaga actttccctt caacgattgc 1440
 gtcgacaaga tgggtgatctg gtgggaggag ggcaagatga cggccaaggt cgtggagtcc 1500
 gccaaaggcca ttctcggcgg cagcaagggtg cgcgtggacc aaaagtgcaa gtcgtccgcc 1560
 cagatcgacc ccacccccgt gatcgtcacc tccaacacca acatgtgcgc cgtgattgac 1620
 gggaacagca ccaccttcga gcaccagcag ccgttcgagg accggatgtt caaatgtgaa 1680
 ctacccgcc gtctggagca cgactttggc aaggtagcga agcaggaagt caaagagttc 1740
 ttccgctggg ccagtgatca cgtgaccgag gtggcgcatg agttctacgt cagaaagggc 1800
 ggagccagca aaagaccgc ccccgatgac gcgatatata gcgagccaa gcgggcctgc 1860
 ccctcagtcg cggatccatc gacgtcagac gcggaaggag ctccgggtgga ctttgccgac 1920
 aggtacaaaa acaaatgttc tcgtcacgcg ggcatgattc agatgctgtt tccctgcaa 1980
 acgtgcgaga gaatgaatca gaatttcaac atttgcttca cacacggggt cagagactgt 2040
 ttagagtgtt tccccggcgt gtcagaatct caaccggctg tcagaaaaaa gacgtatcgg 2100
 aaactctcgc cgattcatca tctgctgggg cgggcgcccg agattgcttg ctcggcctgc 2160
 gacctggtca acgtggacct ggacgactgc gtttctgagc aataaatgac ttaaacagg 2220
 tatggctgcc gatggttatc ttccagattg gctcaggagc aacctctctg agggcattcg 2280
 cgagtgggtg gacctgaaac ctggagcccc gaaacccaaa gccaacagc aaaagcagga 2340
 caacggccgg ggtctggtgc ttcttggtta caagtacctc ggacccttca acggactcga 2400
 caagggggag cccgtcaacg cggcggacgc agcggccctc gagcacgaca aggcctacga 2460
 ccagcagctc aaagcgggtg acaatccgta cctgcggtat aaccacgccg acgccgagtt 2520
 tcaggagcgt ctgcaagaag atacgtcatt tgggggcaac ctcgggcgag cagtcttcca 2580
 ggccaagaag cgggttctcg aacctctcgg tctggttgag gaaggcgcta agacggctcc 2640
 tgcaagaag agaccggtag agccgtcacc tcagcgttcc cccgactcct ccacgggcat 2700
 cggcaagaaa ggccagcagc ccgccagaaa gagactcaat ttcggtcaga ctggcgactc 2760
 agagtcagtc cccgaccctc aacctctcgg agaacctcca gcagcgccct ctagtgtggg 2820
 atctggtaca gtggctgcag gcggtggcgc accaatggca gacaataacg aagggtgccga 2880
 cggagtgggt aatgcctcag gaaattggca ttgcgattcc acatggctgg gcgacagagt 2940
 cattaccacc agcaccgaa cctgggccct gccacctac aacaaccacc tctacaagca 3000
 aatctccagt gaaactgcag gtagtaccac cgacaacacc tacttcggct acagcaccct 3060
 ctgggggtat ttgtacttta acagattcca ctgccacttc tcaccacgtg actggcagcg 3120
 actcatcaac aacaactggg gattccggcc caagaagctg cggttcaagc tcttcaacat 3180
 ccagggtcaag gaggtcacga cgaatgacgg cgttacgacc atcgtaata accttaccag 3240
 cacgattcag gtattctcgg actcgggaata ccagctgccg tacgtcctcg gctctgcgca 3300
 ccagggtgc ctgcctccgt tcccggcgga cgtcttcagt attcctcagt acggctacct 3360
 gactctcaac aatggcagtc agtctgtggg acgttcctcc ttctactgcc tggagtactt 3420
 cccctctcag atgctgagaa cgggcaacaa ctttgagttc agctacagct tcgaggacgt 3480
 gcctttccac agcagctacg cacacagcca gagcctggac cggctgatga atcccccat 3540
 cgaccagtac ttgtactacc tggccagaac acagagtaac ccaggaggca cagctggcaa 3600
 tcgggaactg cagttttacc agggcgggcc ttcaactatg gccgaacaag ccaagaattg 3660
 gttacctgga cttgtcttc ggcaacaaag agtctccaaa acgctggatc aaaacaacaa 3720
 cagcaacttt gcttgactg gtgccaccaa atatcacctg aacggcagaa actcgttggt 3780

taatccccggc gtcgcatg caactcaca ggacgacgag gaccgctttt tcccatccag 3840
 cggagtcctg atttttggaa aaactggagc aactaacaaa actacattgg aaaatgtgtt 3900
 aatgacaaat gaagaagaaa ttcgtcctac taatcctgta gccacggaag aatacgggat 3960
 agtcagcagc aacttacaag cggctaatac tgcagcccag acacaagttg tcaacaacca 4020
 gggagcctta cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcccatctg 4080
 ggccaagatt cctcacacgg atggcaactt tcaccggtct cctttgatgg gcggctttgg 4140
 acttaaacat ccgcctcctc agatcctgat caagaacact cccgttcccg ctaatcctcc 4200
 ggaggtgttt actcctgcc agtttgcttc gtccatcaca cagtacagca ccggacaagt 4260
 cagcgtggaa atcgagtggg agctgcagaa ggaaaacagc aagcgtgga acccggagat 4320
 tcagtacacc tccaactttg aaaagcagac tgggtgtggac tttgccgttg acagccaggg 4380
 tgtttactct gagcctcgcc ctattggcac tcgttacctc acccgtaatc tgtaattgca 4440
 tgtaatacaa taaaccggtt gattcgtttc agttgaactt tggctcctg tgcttcttat 4500
 cttatcggtt tccatagcaa ctggttacac attaaactgct tgggtgcgct tcacgataag 4560
 aacactgacg tcaccgcggt acccctagtg atggagttgg ccactccctc tatgcgcgct 4620
 cgctcgctcg gtggggcctg cggaccaaag gtccgcagac ggcagagctc tgctctgccg 4680
 gccccaccga gcgagcgagc gcgcatagag ggagtggcca a 4721

<210> 181
 <211> 737
 <212> PRT
 <213> capsid protein of adeno-associated virus serotype 7
 <400> 181

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu

565' 570 575
 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735

Leu

<210> 182
 <211> 4393
 <212> DNA
 <213> adeno-associated virus serotype 8

<400> 182
 cagagagggg gtggccaact ccatcactag gggtagcgcg aagcgcttcc cagctgccc 60
 cgtcagcgct gacgtaaatt acgtcatagg ggagtgggtcc tgtattagct gtcacgtgag 120
 tgcttttgcg gcattttgcg acaccacgtg gccatttgag gtatatatgg ccgagtgcgc 180
 gagcaggatc tccattttga ccgcgaaatt tgaacgagca gcagccatgc cgggcttcta 240
 cgagatcgtg atcaagggtg cgagcgacct ggacgagcac ctgccgggca tttctgactc 300
 gtttgtgaac tgggtggcgg agaaggaatg ggagctgccc ccggattctg acatggatcg 360
 gaatctgacg gagcaggcac ccctgaccgt ggcggagaag ctgcagcgcg acttcctggt 420
 ccaatggcgc cgctgtagta aggccccgga ggcctctctc ttgttccagt tcgagaaggg 480
 cgagagctac tttcacctgc acgttctggt cgagaccacg ggggtcaagt ccatggtgct 540
 aggccgcttc ctgagtcaga ttcgggaaaa gcttgggtcca gaccatctac ccgcggggtc 600
 gagccccacc ttgccaact ggttcgcggt gaccaaagac gcggtaatgg cgccggcggg 660
 ggggaacaag gtggtggacg agtgctacat cccaactac ctctgcca agactcagcc 720
 cgagctgcag tgggcgtgga ctaacatgga ggagtatata agcgcgtgct tgaacctggc 780
 cgagcgcaaa cggctcgtgg cgagcacct gaccacgctc agccagacgc aggagcagaa 840
 caaggagaat ctgaaccca attctgacgc gcccgatgc aggtcaaaaa cctccgcgcg 900
 ctatatggag ctggtcgggt ggctggtgga ccggggcatc acctccgaga agcagtggtg 960
 ccaggaggac caggcctcgt acatctcctt caacgcgcgc tccaactcgc ggtcccagat 1020
 caaggccgcg ctggacaatg ccggcaagat catggcgtg accaaatccg cgcccagacta 1080
 cctggtgggg ccctcgtgct ccgcggacat taccagaac cgcatctacc gcatcctcgc 1140

ctctcaatggc tacgaccctg cctacgccgg ctccgtcttt ctgggctggg ctcagaaaaa 1200
 gttcgggaaa cgcaacacca tctggctgtt tggaccgcc accaccggca agaccaacat 1260
 tgcggaagcc atcgcccacg ccgtgccctt ctacggctgc gtcaactgga ccaatgagaa 1320
 ctttcccttc aatgattgag tcgacaagat ggtgatctgg tgggaggagg gcaagatgac 1380
 ggccaaggct gtggagtccg ccaaggccat tctcggcggc agcaagggtg gcgtggacca 1440
 aaagtgaag tcgtccgcc agatcgacc caccctcgtg atcgtcacct ccaacaccaa 1500
 catgtgccc gtgattgacg ggaacagcac cacttcgag caccagcagc ctctccagga 1560
 ccggatgttt aagttcgaac tcaccgccg tctggagcac gactttggca aggtgacaaa 1620
 gcaggaagtc aaagagttct tccgtgggc cagtgtcac gtgaccgagg tggcgcatga 1680
 gttttacgtc agaaagggcg gagccagcaa aagaccgcc ccgatgacg cggataaaag 1740
 cgagcccaag cgggcctgcc cctcagtcgc ggatccatcg acgtcagacg cgggaaggagc 1800
 tccggtggac tttccgcaga ggtacaaaa caaatgttct cgtcacgcgg gcatgcttca 1860
 gatgctgttt ccctgaaaa cgtgcgagag aatgaatcag aatttcaaca tttgcttcac 1920
 acacggggtc agagactgct cagagtgttt ccccgccgtg tcagaatctc aaccggctcgt 1980
 cagaaagagg acgtatcgga aactctgtgc gattcatcat ctgctggggc gggctcccga 2040
 gattgcttgc tcggcctgcg atctgggtcaa cgtggacctg gatgactgtg tttctgagca 2100
 ataaatgact taaaccaggt atggctgccg atggttatct tccagattgg ctcgaggaca 2160
 acctctctga gggcattcgc gagtgggtgg cgctgaaacc tggagccccg aagcccaaag 2220
 ccaaccagca aaagcaggac gacggccggg gtctgggtgct tcctggctac aagtacctcg 2280
 gacccttcaa cggactcgac aagggggagc ccgtcaacgc ggcggacgca gcggccctcg 2340
 agcacgacaa ggcctacgac cagcagctgc aggcgggtga caatccgtac ctgcggtata 2400
 accacgccga cgccgagttt caggagcgtc tgcaagaaga tacgtctttt gggggcaacc 2460
 tcgggcgagc agtcttccag gccaaagaag gggttctcga acctctcggg ctggttgagg 2520
 aaggcgctaa gacggctcct ggaagaaga gaccggtaga gccatcacc cagcgttctc 2580
 cagactcttc tacgggcatt ggcaagaag gccaacagcc cgccagaaaa agactcaatt 2640
 ttggtcagac tggcgactca gactcagttc cagaccctca acctctcggg gaacctccag 2700
 cagcgccctc tgggtgtggg cctaatacaa tggctgcagg cggtggcgca ccaatggcag 2760
 acaataacga aggcgcggac ggagtgggta gttcctcggg aaattggcat tgcgattcca 2820
 catggctggg cgacagagtc atcaccacca gcaccgaac ctggggccctg cccacctaca 2880
 acaaccacct ctacaagcaa atctccaacg ggacatcggg aggagccacc aacgacaaca 2940
 cctacttcgg ctacagcacc ccctgggggt attttgactt taacagattc cactgccact 3000
 tttcaccacg tgactggcag cgactcatca acaacaactg gggattcccg cccaagagac 3060
 tcagcttcaa gctcttcaac atccaggtca aggaggtcac gcagaatgaa ggcaccaaga 3120
 ccattcgcaa taacctcacc agcaccatcc aggtgtttac ggactcggag taccagctgc 3180
 cgtacgttct cggctctgcc caccagggtc gcctgcctcc gttcccggcg gacgtgttca 3240
 tgattcccca gtacggctac ctaacactca acaacggtag tcaggccgtg ggacgctcct 3300
 ccttctactg cctggaatac tttccttcgc agatgtgag aaccggcaac aacttcagt 3360
 ttacttacac cttcgaggac gtgcctttcc acagcagcta cgccacagc cagagcttgg 3420
 accggctgat gaatcctctg attgaccagt acctgtacta cttgtctcgg actcaaaca 3480
 caggaggcac ggcaaatag cagactctgg gcttcagcca aggtgggcct aatacaatgg 3540
 ccaatcaggc aaagaactgg ctgccaggac cctgttaccg ccaacaacgc gtctcaacga 3600
 caaccgggca aaacaacaat agcaactttg cctggactgc tgggacaaa taccatctga 3660
 atggaagaaa ttattgggt aatcctggca tcgctatggc aacacacaaa gacgacgagg 3720
 agcgtttttt tcccagtaac gggatcctga tttttggca acaaaatgct gccagagaca 3780
 atgcggatta cagcagatgtc atgctcacga gcgaggaaga aatcaaaacc actaacctcg 3840
 tggctacaga ggaatacgg atcgtggcag ataacttgca gcagcaaac acggctcctc 3900

aaattggaac tgtcaacagc cagggggcct tacccggtat ggtctggcag aaccgggacg 3960
 tgtacctgca ggggtcccatc tgggccaaga ttcttcacac ggacggcaac ttccaccgt 4020
 ctccgctgat gggcggtctt ggcctgaaac atcctccgcc tcagatcctg atcaagaaca 4080
 cgctgtacc tgcggatcct ccgaccacct tcaaccagtc aaagctgaac tctttcatca 4140
 cgcaatacag caccggacag gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca 4200
 gcaagcgtg gaaccccgag atccagtaca cctccaacta ctacaaatct acaagtgtgg 4260
 actttgtgt taatacagaa ggcgtgtact ctgaaccccg cccattggc acccggtacc 4320
 tcaccgtaa tctgtaattg cctgttaatc aataaaccgg ttgattcgtt tcagttgaac 4380
 ttggtctct gcg 4393

<210> 183
 <211> 738
 <212> PRT
 <213> capsid protein of adeno-associated virus serotype 8
 <400> 183

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
 450 455 460
 Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
 530 535 540
 Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 184
 <211> 735
 <212> PRT
 <213> vp1, clone hu.60

<400> 184

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 185
 <211> 735
 <212> PRT
 <213> vp1, clone hu.61

<400> 185

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Pro Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Arg Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys

580

535

540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 186
 <211> 734
 <212> PRT
 <213> vp1, clone hu.53

<400> 186

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg

130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
 180 185 190
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
 435 440 445
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
 450 455 460
 Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
 465 470 475 480
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
 485 490 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
 500 505 510
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
 515 520 525
 Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
 530 535 540
 Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
 545 550 555 560
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
 565 570 575
 Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
 580 585 590
 Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
 595 600 605
 Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
 610 615 620
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
 625 630 635 640
 Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
 645 650 655
 Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
 660 665 670
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
 675 680 685
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
 690 695 700
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
 705 710 715 720
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730
 <210> 187
 <211> 734
 <212> PRT
 <213> vp1, clone hu.55
 <400> 187
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Gly Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Cys Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
 435 440 445
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
 450 455 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
 465 470 475 480
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg
 500 505 510
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
 515 520 525
 Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
 530 535 540
 Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
 545 550 555 560
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
 565 570 575
 Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
 580 585 590
 Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
 595 600 605
 Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
 610 615 620
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
 625 630 635 640
 Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
 645 650 655
 Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
 660 665 670
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
 675 680 685
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
 690 695 700
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
 705 710 715 720
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730

<210> 188
 <211> 734
 <212> PRT
 <213> vp1, clone hu.54

<400> 188

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140
Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190
Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
195 200 205
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285
Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
405 410 415
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Gly Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
 435 440 445
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
 450 455 460
 Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
 465 470 475 480
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
 485 490 495
 Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Gly
 500 505 510
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
 515 520 525
 Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
 530 535 540
 Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
 545 550 555 560
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
 565 570 575
 Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
 580 585 590
 Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
 595 600 605
 Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp
 610 615 620
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
 625 630 635 640
 Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
 645 650 655
 Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
 660 665 670
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
 675 680 685
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
 690 695 700
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
 705 710 715 720
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730

<210> 189
 <211> 735
 <212> PRT
 <213> vp1, clone hu.49

<400> 189

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Lys Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Gly Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu Tyr Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Ser Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser

"385' 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val His Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 190
 <211> 735
 <212> PRT
 <213> vp1, clone hu.51

<400> 190

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 191
<211> 735
<212> PRT
<213> vp1, clone hu.52

<400> 191

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Arg His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Ser Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Pro Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 192
 <211> 735
 <212> PRT
 <213> vp1, clone hu.56
 <400> 192
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ser Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn

645

650

655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 193
 <211> 734
 <212> PRT
 <213> vp1, clone hu.57
 <400> 193

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Lys
 20 25 30
 Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro Gly
 35 40 45
 Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val
 50 55 60
 Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Arg
 65 70 75 80
 Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
 85 90 95
 Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly Asn
 100 105 110
 Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
 115 120 125
 Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg Pro
 130 135 140
 Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly Lys
 145 150 155 160
 Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
 165 170 175
 Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
 180 185 190
 Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly Ala
 195 200 205
 Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
 210 215 220
 Gly Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile Thr
 225 230 235 240
 Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr

245 250 255
 Lys Gln Ile Ser₂₆₀ Ser Gln Ser Gly Ala₂₆₅ Ser Asn Asp Asn His₂₇₀ Tyr Phe
 Gly Tyr Ser₂₇₅ Thr Pro Trp Gly Tyr₂₈₀ Phe Asp Phe Asn Arg₂₈₅ Phe His Cys
 His Phe₂₉₀ Ser Pro Arg Asp Trp₂₉₅ Gln Arg Leu Ile Asn₃₀₀ Asn Asn Trp Gly
 Phe Arg Pro Lys Arg Leu₃₁₀ Asn Leu Lys Leu Phe₃₁₅ Asn Ile Gln Val Lys₃₂₀
 Glu Val Thr Gln Asn₃₂₅ Asp Gly Thr Thr Thr₃₃₀ Ile Ala Asn Asn Leu₃₃₅ Thr
 Ser Thr Val Gln₃₄₀ Val Phe Thr Asp Leu₃₄₅ Glu Tyr Gln Leu Pro₃₅₀ Tyr Val
 Leu Gly Ser₃₅₅ Ala His Gln Gly Cys₃₆₀ Leu Pro Pro Phe Pro₃₆₅ Ala Asp Val
 Phe Met₃₇₀ Val Pro Gln Tyr Gly₃₇₅ Tyr Leu Thr Leu Asn₃₈₀ Asn Gly Ser Gln
 Ala Val Gly Arg Ser₃₉₀ Ser Phe Tyr Cys Leu Glu₃₉₅ Tyr Phe Pro Ser Gln₄₀₀
 Met Leu Arg Thr Gly₄₀₅ Asn Asn Phe Thr Phe₄₁₀ Ser Tyr Thr Phe Glu₄₁₅ Asp
 Val Pro Phe His₄₂₀ Ser Ser Tyr Ala His₄₂₅ Ser Gln Ser Leu Asp₄₃₀ Arg Leu
 Met Asn Pro₄₃₅ Leu Ile Asp Gln Tyr₄₄₀ Leu Tyr Tyr Leu Ser₄₄₅ Arg Thr Asn
 Thr Pro Ser Gly Thr Thr Thr₄₅₅ Gln Ser Arg Leu Gln₄₆₀ Phe Ser Gln Ala
 Gly Ala Ser Asp Ile Arg₄₇₀ Asp Gln Ser Arg Asn₄₇₅ Trp Leu Pro Gly Pro₄₈₀
 Cys Tyr Arg Gln Gln₄₈₅ Arg Val Ser Lys Thr₄₉₀ Ala Ala Asp Asn₄₉₅ Asn Asn
 Gly Glu Tyr Ser₅₀₀ Trp Thr Gly Ala Thr₅₀₅ Lys Tyr His Leu Asn₅₁₀ Gly Arg
 Asp Ser Leu₅₁₅ Val Asn Pro Gly Pro₅₂₀ Ala Met Ala Ser His₅₂₅ Lys Asp Asp
 Glu Glu₅₃₀ Lys Phe Phe Pro Gln₅₃₅ Ser Gly Val Leu Ile₅₄₀ Phe Gly Lys Gln
 Gly Ser Glu Lys Thr Asn₅₅₀ Val Asp Ile Glu Lys₅₅₅ Val Met Ile Thr Asp₅₆₀
 Glu Glu Glu Ile Arg₅₆₅ Thr Thr Asn Pro Val₅₇₀ Ala Thr Glu Gln Tyr₅₇₅ Gly
 Ser Val Ser Thr₅₈₀ Asn Leu Gln Ser Gly₅₈₅ Asn Thr Arg Ala Ala₅₉₀ Thr Ser
 Asp Val Asn₅₉₅ Thr Gln Gly Val Leu₆₀₀ Pro Gly Met Val Trp₆₀₅ Gln Asp Arg

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
 610 615 620
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
 625 630 640
 Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
 645 650 655
 Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
 660 665 670
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
 675 680 685
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
 690 695 700
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
 705 710 715 720
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730
 <210> 194
 <211> 735
 <212> PRT
 <213> vp1, clone hu.58
 <400> 194
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asp His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Asp Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Arg Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Ile Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ser Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Arg Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 195
 <211> 735
 <212> PRT
 <213> vp1, clone hu.63
 <400> 195
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Pro Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 196
 <211> 735
 <212> PRT
 <213> vp1, clone hu.64

<400> 196

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu His Ser Leu Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155
 Lys Ala Gly Gln Gln Pro Ala Arg Arg Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly

500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 197
 <211> 738
 <212> PRT
 <213> vp1, clone hu.66

<400> 197

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ala Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Glu Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Cys Ala His Ser Gln Ser
 420 425 430
 Ser Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Arg Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 198
 <211> 738
 <212> PRT
 <213> vp1, clone hu.67

<400> 198

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Leu
 35 40 45

WO 2005/033321

Gly Tyr Lys Tyr Leu Gly Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415

WO 2005/033321

Thr Phe Glu Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
 580 585 590
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735
 Asn Leu

<210> 199
 <211> 2175
 <212> DNA
 <213> adeno-associated virus serotype 5

<400> 199

atgtcttttg ttgatcacc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60
 tttttggggc ttgaagcggg cccaccgaaa ccaaaacca atcagcagca tcaagatcaa 120
 gccctggttc ttgtgctgcc tgggtataac tatctcggac ccggaacagg tctcgatcga 180
 ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240
 cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300
 gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360
 aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccttacc 420
 ggaaagcggg tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480
 aagccttcca cctcgtcaga cgccgaagct ggaccagcg gatcccagca gctgcaaatc 540
 ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600
 ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660
 gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720
 agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780
 aacgcctact ttggatacag caccctctgg gggtaacttg actttaaccg cttccacagc 840
 cactggagcc cccgagactg gcaaagactc atcaacaact actggggcct cagaccccg 900
 tccctcagag tcaaatctt caacattcaa gtcaaaggagg tcacggtgca ggactccacc 960
 accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020
 ctgcccacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080
 tttacgctgc cgagtagcgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140
 gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200
 aactttgagt ttacctacaa ctttgaggag gtgccccttc actccagctt cgctccaggt 1260
 cagaacctgt tcaagctggc caaccgctg gtggaccagt acttgaccg cttcgtgagc 1320
 acaataaca ctggcggagt ccagttcaac aagaacctg ccgggagata cgccaacacc 1380
 tacaaaaact ggttcccggg gcccatgggc cgaaccagg gctggaacct gggctccggg 1440
 gtcaaccgcg ccagtgtcag gccttctgcc acgaccaata ggatggagct cgaggcgcg 1500
 agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560
 tatgccctgg agaactat gatcttcaac agccagccgg cgaaccggg caccaccgcc 1620
 acgtacctcg agggcaacat gctcatcacc agcagagcgc agacgcagcc ggtgaaccgc 1680
 gtggcgatca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc 1740
 gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800
 gtgtacctcc aaggacctat ctgggccaa atccagaga cgggggcgca ctttcacccc 1860
 tctccggcca tgggcggatt cggactcaaa caccaccgc ccatgatgct catcaagaac 1920
 acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980
 cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040
 aagagggtga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100
 tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160
 acccgacccc ttttaa 2175

<210> 200
 <211> 2211
 <212> DNA
 <213> adeno-associated virus, serotype 3-3

<400> 200
 atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60
 gagtggtggg ctctgaaacc tggagtccct caaccctaa cgaaccaaca acaccaggac 120
 aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gaccgggtaa cggactcgac 180
 aaaggagagc cggtaacga ggcggacgcg gcagccctcg aacacgaca agcttacgac 240
 cagcagctca aggcgggtga caaccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360
 gccaaaaaga ggatccttga gcctcttggg ctggttgagg aagcagctaa aacggctcct 420
 ggaaagaagg gggctgtaga tcagtctcct caggaaccgg actcatcatc tgggtgtggc 480
 aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag 540
 tcagtccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600
 aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcca cagagtcac 720
 accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatac 780
 tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840
 tattttgact ttaacagatt cactgcccac ttctcaccac gtgactggca gcgactcatt 900
 aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960
 agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020
 caagtgttta cggactcggg gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080
 tgtctcccg cgtttccagc ggacgtcttc atggtccctc agtatggata cctcacctg 1140
 aacaacggaa gtcaagcggg gggacgctca tctttttact gcctggagta cttcccttcg 1200
 cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260
 cacagcagct acgctcacag ccagagtgtg gatcgcttga tgaatcctct tattgatcag 1320
 tatctgtact acctgaacag aacgcaagga acaacctctg gaacaacca ccaatcacgg 1380
 ctgcttttta gccaggctgg gcctcagctc atgtctttgc aggccagaaa ttggctacct 1440
 gggccctgct accggcaaca gagactttca aagactgcta acgacaaca caacagtaac 1500
 tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560
 ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620
 ctaatatattg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680
 acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaaactgtg 1740
 gcaaataact tgcagagctc aaatacagct cccacgactg gaactgtcaa tcatcagggg 1800
 gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860
 aagattcctc acacggatgg acactttcat cttctcctc tgatgggagg ctttgactg 1920
 aaacatccgc ctctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980
 actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040
 gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100
 tacacttcca actacaaca gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160
 tatagtgaac ctgcctctat tggaaaccgg tatctcacac gaaacttgta a 2211

<210> 201
 <211> 2205
 <212> DNA
 <213> adeno-associated virus, serotype 4-4

<400> 201
 atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60
 tgggtggcgc tgcaacctgg agccccctaaa cccaaggcaa atcaacaaca tcaggacaac 120
 gctcggggtc ttgtgcttcc ggggttcaaaa tacctcggac ccggcaacgg actcgacaag 180
 ggggaacctg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240
 cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300
 cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360
 aaaaagaggg ttcttgaacc tcttgggtctg gttgagcaag cgggtgagac ggctcctgga 420
 aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480
 aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540
 ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgatg gcgtgcagca 600

```

" gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660
gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720
tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780
aacacctaca acggattctc cccccctgg ggatactttg acttcaaccg cttccactgc 840
cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900
gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960
acaacggtgg ctaataacct taccagcacg gtccagatct ttgaggactc gtcgtacgaa 1020
ctgccgtacg tgatggatgc ggggtcaagag ggcagcctgc ctctttttcc caacgacgtc 1080
tttatggtgc ccagtagcgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140
actgacagaa atgccttcta ctgcctggag tacttttctt cgagatgct gcggactggc 1200
aacaactttg aaattacgta cagttttgag aagggtgcctt tccactcgat gtacgcgcac 1260
agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320
tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380
cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440
cagggcttct caaagactgc caatcaaac tacaagatcc ctgccaccgg gtcagacagt 1500
ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560
cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620
gcggggccta aacagaacgg caacacggcc accgtaccgg ggactctgat cttcacctct 1680
gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740
ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800
cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860
cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920
ccgcctcttc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980
agctctactc cggtaaactc cttcattact cagtacagca ctggccagggt gtcggtgcag 2040
attgactggg agatccagaa ggagcgggcc aaacgctgga accccgagggt ccagtttacc 2100
tccaactacg gacagcaaaa ctctctgttg tgggtctccg atgaggctgg gaaatacact 2160
gagcctaggg ctatcggtag ccgtacctc acccaccacc tgtaa 2205

```

```

<210> 202
<211> 2211
<212> DNA
<213> adeno-associated virus, serotype 1

```

```

<400> 202
atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgtgtgg acttgaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgtgtct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcttc gggcatcggc 480
aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgtgc tgtgggacct 600
actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720
accaccagca ccgcacctg ggccttgccc acctacaata accacctcta caagcaaadc 780
tccagtgcct caacgggggc cagcaacgac aaccactact tcggctacag cccccctgg 840
gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

```



```

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960
gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020
gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080
ggctgcctcc ctccgttccc ggcggacgtg ttcattgattc cgcaatacgg ctacctgacg 1140
ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200
tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260
ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320
caatacctgt attacctgaa cagaactcaa aatcagtcg gaagtgccca aaacaaggac 1380
ttgtgtttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500
tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560
ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcgggtgc 1620
atgatttttg gaaaagagag cgccggagct tcaaactctg cattggacaa tgtcatgatt 1680
acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740
gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800
gcattacctg gcatgggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggac 1860
aaaattcctc acacagatgg acactttcac ccgtctctc ttatgggcgg ctttggactc 1920
aagaacccgc ctctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980
gagttttcag ctacaaagt ttgcttcattc atcacccaat actccacagg acaagtgagt 2040
gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100
tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcaccctg taccttaccg gtcccctgta a 2211

```

```

<210> 203
<211> 2211
<212> DNA
<213> adeno-associated virus, serotype 6

```

```

<400> 203
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggccctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgct tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420
ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480
aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg acccacaacc tctcggagaa cctccagcaa ccccgcctgc tgtgggacct 600
actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcac 720
accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatac 780
tccagtgcct caacgggggc cagcaacgac aaccactact tcggctacag caccctctgg 840
gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900
atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960
gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020
gttcaagtct tctcggactc ggagtaccag ttgcccgtac tcctcggctc tgcgcaccag 1080
ggctgcctcc ctccgttccc ggcggacgtg ttcattgattc cgagctacgg ctacctaacg 1140
ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

```

```

tcgcagatgc tgagaacggg caataacttt acccttcagct acaccttcga ggacgtgcct 1260
ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320
cagtacctgt attacctgaa cagaactcag aatcagtcgg gaagtgccca aaacaaggac 1380
ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440
ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500
tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560
ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcgggtgc 1620
atgatttttg gaaaggagag cgccggagct tcaaactctg cattggacaa tgtcatgatc 1680
acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740
gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800
gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860
aaaattcctc acacggatgg acactttcac ccgtctctc tcattgggcgg ctttggactt 1920
aagcaccgcg ctctcagat cctcatcaaa aacacgcctg ttcttgcgaa tcctccggca 1980
gagttttcgg ctacaaagt tgccttcttc atcaccagc attccacagg acaagtgcgc 2040
gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100
tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcaccgt tacctcacc gtcccctgta a 2211

```

```

<210> 204
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.63

```

```

<400> 204
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaaag ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac 180
aaggagagag cggtcacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccgtac cccaagtaca accacgccga gcgaggttc 300
caggagcgtc taaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
gcgaaaaaga ggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctc gcggagccag actctctctc gggaaccgga 480
aaagcgggac agcagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540
tccgtacctg accccagacc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgagg gcgcgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggca cagagtcac 720
accaccagca cccgcacctg ggctctgcc acctacaaca accacctta caagcagatt 780
tccagccaat caggagctc aaacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt cactgccac ttttcgccac gtgactggca aagactcatc 900
aacaacaatt ggggattccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960
aaggagggtc cgcagaatga cggtagcag acgattgcca ataacctac cagcacggtt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcttccgc cgttccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttcttct 1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca ctttgagga cgttcttct 1260
cacagcagct acgcccacag ccagagttag gaccgtctca tgaatctct catcgaccag 1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgca gtcaaggctt 1380
cagttttctc aggcgggagc aagtgcatt cgggaccagt ctaggaaact gcttcttgg 1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

```

tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc 1560
 ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttccctcagag cggggttctc 1620
 atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca 1680
 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
 ctccagga tggtgtggca ggacagagac gtgtacctgc aggggcccac ctgggcaaaag 1860
 attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920
 caccctcccc cgagattct catcaagaac accccggtag ctgcgaatcc ttcgactacc 1980
 ttcagtgcgg caaagtttgc ttcttcatt acacagtact ccacggggca ggtcagcgtg 2040
 gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtag 2100
 acttccaact acaacaaatc tgtaatgtg gactttactg tggacactaa tgggtgtgtat 2160
 tcagagcctc gccccattgg caccaggtag ctgactcgta atctgtaa 2208

<210> 205

<211> 2208

<212> DNA

<213> new AAV serotype, clone hu.56

<400> 205

atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggccaccca ccaccaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctggatac aagtacctcg gaccttcaa cggactcgac 180
 aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
 cggcagctcg acagcggaga caaccgtag ctcaagtaca accacgccga cgcggagttt 300
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaaccgga 480
 aaagcgggca accagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540
 tccgtacctg acccccagcc tctcggacag ccaccagcat cccctctggt tctgggaact 600
 aatacagatg ctacaggcag tggcgacca atggcagaca ataacgaggg cgcgcagga 660
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggca cagagtcgtc 720
 accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcagatt 780
 tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840
 tattttgact tcaacagatt ccactgccac ttttcgccac gcgactggca gagactcatc 900
 aacaacaact ggggattccg gcccaaaaga ctcaacttca agctgtttaa cattcaagtc 960
 aaggaggtca cgcagaatga cggtagcag acgattgcca ataaccttac cagcacggtt 1020
 cagggtgtta ctgacttggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggga gtcaggcggg aggacgctct tccttttact gcctggagta ctttccttct 1200
 cagatgcttc gcaccggaaa caactttacc ttcagctaca cttttgaaga cgttcctttc 1260
 cacagcagct acgttcacag tcaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcag aacaaacact ccaagcggaa ccactacgca gtccaggctt 1380
 cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440
 ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaaca cagtgaatac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
 ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttccctcaaag cggggttctc 1620
 atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680
 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

ctcccaggca tggctctggca ggacagagac gtgtacctgc aggggcccac ctgggcaaaa 1860
 attccacaca cggacggaca ttttcacccc tctccccca tggcgggatt tggacttaaa 1920
 caccctcttc cacagattct cattaagaat accccggtag ctgcgaatcc ttcgaccacc 1980
 ttcagcgcgg caaagtttgc ttccttcac acacagtatt ccacggggca ggtcagcgtg 2040
 gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtag 2100
 acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tggggtgtat 2160
 tcagagcctc gccctatttg caccagatac ctgactcgta atctgtaa 2208

<210> 206
 <211> 2205
 <212> DNA
 <213> new AAV serotype, clone hu.57

<400> 206
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaagaccgc cagagcggca taaggacgac 120
 agcaggggtc ttgtgcttcc tggatacaag tacctcggac cttcaacgg actcgacaag 180
 ggagagccgg tcaacgaggg agacgccgcg gccctcagac acgacaaggc ctacgaccgg 240
 cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgccgacgc ggagtttcag 300
 gagcgcccta aagaagatac gtcttttggg ggcaacctcg gacgagcagt cttccaggcg 360
 aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac ggctccggga 420
 aaaaagaggg ccgtagagca ctctcctgtg gagccagact cctcctcggg aaccggaaaa 480
 gcgggcaacc agcctgcaag aaaaagattg aatttcggtc agactggaga cgcagactcc 540
 gtacctgacc ccagcctct cggacagcca ccagcagccc cctctggtct gggaaactaat 600
 acgatggcta caggcagtag cgcaccaatg gcagacaata acgagggcgc cgacggagtg 660
 ggtaattcct cgggagattg gcattgcgat tccacatgga tggcgacag agtcattacc 720
 accagcacc gcacctgggc cctgcccacc tacaacaacc acctctaca gcagatttcc 780
 agccaatcag gagccagcaa tgacaaccac tactttggct acagcaccac ttgggggtat 840
 tttgacttca acagattcca ctgccacttt tcgccacgcg actggcagag actcatcaac 900
 aacaactggg gattccggcc caaaagactc aacctcaagc tgtttaacat tcaagtcaag 960
 gaggtcacgc agaattgacg tacgacgacg attgccaata accttaccag cacggttcag 1020
 gtgtttactg acttgagat ccagctcccg tacgtcctcg gctcggcgca tcaaggatgc 1080
 ctcccgccgt tcccagcaga cgtcttcatt gtgccacagt atggatacct caccctgaac 1140
 aacgggagtc aggcggtagg acgtcttccc ttttactgcc tggagtactt tccttctcag 1200
 atgcttcgta ccggaaacaa ctttaccttc agctacactt ttgaagacgt tcctttccac 1260
 agcagctacg ctacagtc aagtctggac cgtctcatga atcctctcat cgaccagtag 1320
 ctgtattact tgagcagaac aaacactcca agcgggaacca ctacgcagtc caggcttcag 1380
 ttttctcagg ccggagcgag tgacattcgg gaccagtcta ggaactggct tcctggacct 1440
 tgttaccgcc agcagcgagt atcaaagaca gctgcggata acaacaacgg tgaatactcg 1500
 tggactggag ctaccaagta ccacctcaat ggcagagact ctctggtgaa tccgggcccg 1560
 gccatggcca gccacaagga cgatgaagaa aagtttttct ctcaaagcgg ggttctcatc 1620
 tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggctcat gattacagac 1680
 gaagaggaaa tcaggaccac caatcccgtg gctacggagc agtatggttc tgtatctacc 1740
 aacctccaga gcggcaacac acgagcagct acctcagatg tcaacacaca aggcgttctt 1800
 ccaggcatgg tctggcagga cagagacgtg tacctgcagg gggccatctg ggcaaaaatt 1860
 ccacacacgg acggacattt tcacccctct cccctcatgg gcggatttgg acttaaacac 1920
 cctcctccac agattctcat taagaatacc ccggtacctg cgaatccttc gaccaccttc 1980
 agcgcggcaa agtttgcttc ctcatcaca cagtattcca cggggcaggt cagcgtggag 2040
 atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaat tcagtacact 2100

tccaactaca acaaatctgt taatgtggac' tttactgtgg acactaatgg ggtgtattca 2160

gagcctcgcc ctattggcac cagatacctg actcgtaatc tgtaa 2205

<210> 207
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.58

<400> 207
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtacg accacgccga cgcggagttt 300
caggagcgcc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaaccga 480
aaagcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacgtatg ctacaggcag tggcgacca atggcagaca ataacgatgg cgcgcagga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca ccgaacctg ggtctgccc acctacaaca accatctgta caagcagatt 780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960
agagaggtca cgcagaatga tggtagcagc acgattgcca ataaccttac cagcacggtt 1020
cagggtgtta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgctcccgcc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta cttcccttct 1200
cagatgtctg gtaccggaaa caactttacc ttcagctaca cttttgagga tggtcctttc 1260
cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaact ccaagcggaa ccaccacgca gtccaggctt 1380
cagttttctc aggccggagc gagtgcatt cgggacagt ctaggaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg acaacaaca cagtgaatac 1500
tcgtggattg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggcaatgg ccagccacaa ggacgatgaa gaaaagtgtt ttctcagag cggggttctc 1620
atctttggaa aacaaggatc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
gacgaagagg aatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca tctactgcag atgtcaacac acaaggcggt 1800
cttccaggca tggctctggc ggacagagac gtgtacctgc aggggcctat ctgggcaaag 1860
attccgcaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa 1920
caccctcctc cacagattct catcaaaaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtgtgc ttccttcac acacagtatt ccacggggcg ggtagcgtg 2040
gagatcgagt gggagctaca gaaggagaac agcaaagcgt ggaatcccga gatccagtac 2100
acttccaact acaaaaatc tgtaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 208
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.51

<400> 208
 atggctgccg atggttatct tccagattgg ctccaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtaacctg gaccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
 gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgtcaa gacggctcca 420
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
 aaggcggggc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
 tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
 aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgcgcagcga 660
 gtgggttaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
 tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
 tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
 aacaacaact ggggatttcg acccaagaga ctcaacttca agtctttta cattcaagtc 960
 aaagaggta cgcagaatga cggtagcagc acgattgcc aataacctac cagcacgggt 1020
 cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgcttccgc cgttccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggga gtcaggcagt aggacgtct tcatcttact gcctggagta ctttcttct 1200
 cagatgctgc gtaccgga acaactttacc ttcagctaca cttttgagga cgttcctttc 1260
 cacagcggct acgtctcacg ccagagtctg gaccgtctca tgaatcctc catcgaccag 1320
 tacctgtatt acttgagcac acaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380
 cagttttctc aggcgggagc gagtgacatt cgggaccagt ctaggaactg gcttctgga 1440
 ccctgttacc gccagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
 tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
 ccggccatgg caagccacaa ggacaatgaa gaaaagtgtt ttcctcagag cggggttctc 1620
 atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
 gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtacgg ttctgtatct 1740
 accaacttc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcgtt 1800
 cttccaggca tgggtctggca ggacagagat gtgtacctc aggggcccac ctgggcaaag 1860
 attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaa 1920
 caccctctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
 ttcagtgcgg caaagtgtgc ttccttcac acacagtact ccacgggaca ggtcagcgtg 2040
 gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccg aattcagtac 2100
 acttccaact acaacaagtc tgtaaatgtg gactttactg tggactacta tggcgtgtat 2160
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 209
 <211> 2208
 <212> DNA
 <213> new AAV serotype, clone hu.49

<400> 209
 atggctgccg atggttatct tccagattgg ctcaaggaca ctctctctga aggaataaga 60
 cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac 120
 gacagcaggg gtcttgtgct tcctgggtac aagtaacctg gaccttcaa cggactcgac 180
 aagggagagc cggtaacga ggcagacgcc gcggccctcg agtacgacaa ggccctacgac 240
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300

```

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctct gtggagccag actcctcctc gggaacagga 480
aaagcggggc agcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatc 780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaggagggtca cgcagaatga cggtagcagc acgattgcc aataacctac cagcacgggt 1020
cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc ccggctcggc gcatcaagga 1080
tgctctccgc cgttccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140
aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttcttct 1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca ctttgagga tgctcttct 1260
cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctaggaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag cgggggttctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac acaaggcgtt 1800
cttcaggca tggcttgga ggacagagac gtgcacctgc aggggcctat ctgggcaaa 1860
attccacaca cggacggaca ttttcacccc tctcccccta tgggcggatt tggacttaa 1920
caccctctc cacagattct catcaagaac accccgttac ctgcaaatcc ttcgaccacc 1980
ttcagtgcgg caaagtttgc ttccttcac acacagtatt ccacagggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgtt ggaaccccga gatccagtac 2100
acttccaact acaacaatc tgtaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 210
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.52

```

```

<400> 210
atggctgccc atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaacc tggccacca ccacaaagc ccgacagagc gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gacccttcaa cgactcgac 180
aaggagagc cggctcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctct gtggagccag actcctcctc gggaaccgga 480
aaggcggggc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600

```

```

aatac gatg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa tcggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta cagacaaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggatttcg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggcca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacggtt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccgc cgttcccagc agacgtcttc atgggtgccac agtatggata cctcaccctg 1140
agcaacggga gtcaggcagt aggacgtctt tcattttact gcccggagta ctttccttct 1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260
cacagcagct acgtcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcac aacaaacct ccaagtggaa ccaccacgca gtcaaggctt 1380
cagttttctc aggccggagc gagtgcatt cgggaccagt ctaggaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cgggggttctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcggt 1800
cttcaggga tggctcggca ggacagagat gtgtaccttc agggggccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctca tgggtggatt cggacctaaa 1920
cacctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacgggaca ggtcagcgtg 2040
gagatcagat gggagctgca gaaggaaaac agcaaacgct ggaatccga aattcagtac 2100
acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atttgtaa 2208

```

```

<210> 211
<211> 2208
<212> DNA
<213> adeno-associated virus, serotype 2

```

```

<400> 211
atggctgccg atgggtatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaac tggcccacca ccaccaaac cgcagagcg gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aaggagagc cggtaacga ggcagcgcc gcggccctcg agcacgaca agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
aaggcgggac agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggaact 600
aatac gatg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

```


aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcttcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcagc aggcgctct tcattttact gcctggagta ctttccttct 1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaacact ccaagtggaa ccaccacgca gtcaaggcct 1380
cagttttctc aggccggagc gagtgcatt cgggaccagt ctaggaactg gcttcctgga 1440
ccctgttacc gccagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctacaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttctcagag cggggttctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcgtt 1800
cttcaggca tggctcggca ggacagagat gtgtacctc agggggccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctca tgggtggatt cggacttaaa 1920
caccctctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacgggaca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggaaaac agcaaagcgt ggaatcccga aattcagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 212
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.64

<400> 212
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agtcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctg gacccttcaa cggactcgac 180
aaggagagc cggtaacga ggacagcgc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acggcggaga caaccgtac ctcaagtaca accacgccga cgcggagtct 300
caggagcgtc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
gcgaaaaaga ggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggcgggtaga gactctctt gcggagccag actcctcctc ggaaccgga 480
aaagcgggcc agcagcctgc aagaaggaga ttgaatttcg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgaggg cgcgcagga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caggcagatt 780
tccagccaat caggagctc aaacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt cactgccac ttttcgccac gtgactggca aagactcatc 900
aacaacaatt ggggatcccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960
aaggagggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcttcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcagc aggcgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccgga aa caactttacc ttcagctaca cctttgagga cgttcctttc 1260
 cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct cgtcgaccag 1320
 tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggcct 1380
 cagttttctc aggccggagc aagtgcattt cgggaccagt ctaggaaactg gcttccttga 1440
 ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
 tcgtggactg gagctacca gtaccacctt aatggaagag actctctggt gaatccgggc 1560
 ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620
 atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg catgattaca 1680
 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
 cttccaggca tgggtgtggca ggacagagac gtgtacctgc aggggcccac ctgggcaaaag 1860
 attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa 1920
 caccctcccc cgagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc 1980
 ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040
 gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac 2100
 acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 213
 <211> 2214
 <212> DNA
 <213> adeno-associated virus, serotype 7

<400> 213
 atggctgccg atggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
 gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
 aacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgaca ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttcag 360
 gccagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
 gcaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcac 480
 ggcaagaag gccagcagcc cgccagaag agactcaatt tcggtcagac tggcgactca 540
 gagtcagtcc ccgacctca acctctcggg gaacctccag cagcgccctc tagtgtggga 600
 tctggtacag tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 attaccacca gcacccgaac ctggggccctg cccacctaca acaaccacct ctacaagcaa 780
 atctccagt aaactgcagg tagtaccac gacaacacct acttcggcta cagcaccccc 840
 tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900
 ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc 960
 caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020
 acgattcagg tattctcggg ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080
 cagggctgcc tgccctcgtt cccggcgagc gtcttcatga ttcctcagta cggtacactg 1140
 actctcaaca atggcagtc gtctgtggga cgttcctcct tctactgcct ggagtacttc 1200
 cctctctaga tgctgagaac gggcaacaac tttgagttca gctacagctt cgaggacgtg 1260
 cttttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tccccctatc 1320
 gaccagtact tgtactacct ggccagaaca cagagtaacc caggaggcac agctggcaat 1380
 cgggaactgc agttttacca gggcgggcct tcaactatgg ccgaacaagc caagaattgg 1440
 ttacctggac ctgtctccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac 1500

```

agcaactttg cttggactgg tgccacaaa tatcacctga acggcagaaa ctcgttggtt 1560
aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620
ggagtctctga tttttgaaa aactggagca actaacaaaa ctacattgga aaatgtgtta 1680
atgacaaatg aagaagaaat tcgtcctact aatcctgtag ccacggaaga atacgggata 1740
gtcagcagca acttacaagc ggctaatact gcagcccaga cacaagttgt caacaaccag 1800
ggagccttac ctggcatggg ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860
gccaagattc ctcacacgga tggcaacttt caccctctc ctttgatggg cggctttgga 1920
cttaaacatc cgctcctca gatcctgac aagaacactc ccgttcccgc taatcctccg 1980
gagggtgttta ctctgcca gtttgcttcg ttcacacac agtacagcac cggacaagtc 2040
agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgtggaa cccggagatt 2100
cagtacacct ccaactttga aaagcagact ggtgtggact ttgccgttga cagccagggt 2160
gtttactctg agcctcgccc tattggcact cgttacctca ccgtaaatct gtaa 2214

```

```

<210> 214
<211> 2217
<212> DNA
<213> adeno-associated virus, serotype 8

```

```

<400> 214
atggctgccc atggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60
gagtgggtgg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctgc aggcgggtga caatccgtac ctgcgtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaga gaccggtaga gccatcacc cagcgttctc cagactctc tacgggcatc 480
ggcaagaagc gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540
gagtcagttc cagaccctca acctctcggg gaacctccag cagcgcctc tgggtgtgga 600
cctaatacaa tggctgcagg cgggtggcga ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcaccgaac ctgggcccgt cccacctaca acaaccacct ctacaagcaa 780
atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt taacagattc cactgccact ttaccacag tgactggcag 900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960
atccagggtc aggaggtcac gcagaatgaa ggcaccaaga ccacgcgcaa taacctcacc 1020
agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080
caccagggtc gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140
ctaactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200
tttcttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260
gtgcctttcc acagcagcta cgccacagc cagagcttgg accggctgat gaatcctctg 1320
attgaccagt acctgtacta cttgtctcgg actcaaaca caggaggcac ggcaaatacg 1380
cagactctgg gtttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440
ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500
agcaactttg cctggactgc tgggacaaa taccatctga atggaagaaa ttcattggct 1560
aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620
gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680
atgctcacca gcgaggaaga aatcaaaacc actaacctg tggctacaga ggaatacggg 1740
atcgtggcag ataacttgca gcagcaaac acggctctc aaattggaac tgtcaacagc 1800

```

cagggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggccccatc 1860
 tgggccaaga ttccctcacac ggacggcaac ttccaccctg ctccgctgat gggcggcttt 1920
 ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980
 ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040
 gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgtg gaaccccag 2100
 atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160
 ggcgtgtact ctgaaccccg cccattggc acccggtacc tcaccgtaa tctgtaa 2217

<210> 215
 <211> 2217
 <212> DNA
 <213> new AAV serotype, clone hu.67

<400> 215
 atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
 gagtgggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120
 gacggccggg gtctgggtgct tcttggttac aagtacctg gacccttcaa cggactcgac 180
 aagggggagc ccgtcaatgc ggcggacgca gcgccctcg agcacgacaa ggcctacgac 240
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag 360
 gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
 ggaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
 ggcaagaaag gccagcagcc cgtaaaaaag agactgaact ttggtcagac tggcgactca 540
 gagtcagtc ccgacctca accaatcgga gaaccaccag caggccctc tggctcggga 600
 tctggtacaa tggtgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660
 ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
 atcaccacca gacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780
 atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
 ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
 cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
 atccaggcca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
 agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080
 caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
 cttactactga acaatggaag tcaagccgta ggccgttcct cttctactg cctggaatat 1200
 tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260
 gtgcctttcc acagcggcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
 atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380
 cagcaattgt tattttctca agctgggcct gcaaacaatgt cggctcaggc taagaactgg 1440
 ctacctggac cttgtaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500
 agcaactttg cttggactgg tgccaccaa taccacctga acggaagaga ctctttggtg 1560
 aatcccgggt tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcagat 1620
 ggagtcctga tgtttgaaa acaggggtgt ggaagagaca atgtggacta cagcagcgtt 1680
 atgctaacca gcgaagaaga aattaaaacc actaacctg tagccacaga acaatacgg 1740
 gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
 caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggccccatc 1860
 tgggccaaga ttccctcacac ggacggcaac ttccaccctt caccgctaata gggaggattt 1920
 ggactgaagc acccacctcc tcagatcctg atcaagaaca cgcgggtacc tgcggatcct 1980
 ccaacgacgt tcagccaggc gaaattggct tccttcatta cgagtacag caccggacag 2040
 gtcagcgtgg aaatcgagt ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaattgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccatgtgg actcgttacc tcacccgtaa tctgtaa 2217

<210> 216

<211> 724

<212> PRT

<213> vp1, serotype 5

<400> 216

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
 325 330 335
 Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
 340 345 350
 Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
 355 360 365
 Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
 370 375 380
 Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
 385 390 395 400
 Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
 405 410 415
 Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
 420 425 430
 Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
 435 440 445
 Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
 450 455 460
 Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
 465 470 475 480
 Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
 485 490 495
 Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
 500 505 510
 Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
 515 520 525
 Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
 530 535 540
 Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
 545 550 555 560
 Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
 565 570 575
 Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
 580 585 590
 Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
 595 600 605
 Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
 610 615 620
 Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
 625 630 635 640
 Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
 645 650 655
 Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
 660 665 670
 Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln

675

680

685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 217
<211> 736
<212> PRT
<213> vp1, serotype 3-3
<400> 217

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
130 135 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His

275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
 435 440 445
 Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
 450 455 460
 Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
 485 490 495
 Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
 500 505 510
 Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
 515 520 525
 Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
 530 535 540
 Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
 565 570 575
 Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
 580 585 590
 Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
 705 710 715 720
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

 <210> 218
 <211> 734
 <212> PRT
 <213> vp1, serotype 4-4

 <400> 218
 Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
 1 5 10 15
 Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
 20 25 30
 Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
 35 40 45
 Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
 50 55 60
 Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
 65 70 75 80
 Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
 85 90 95
 Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
 100 105 110
 Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
 115 120 125
 Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
 130 135 140
 Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
 145 150 155 160
 Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
 165 170 175
 Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
 180 185 190
 Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
 195 200 205
 Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
 210 215 220
 Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
 225 230 235 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
 245 250 255
 Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
 260 265 270
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
 275 280 285
 Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
 290 295 300
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
 305 310 315 320
 Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
 325 330 335
 Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
 340 345 350
 Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
 355 360 365
 Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
 370 375 380
 Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
 385 390 395 400
 Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
 405 410 415
 Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
 420 425 430
 Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
 435 440 445
 Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
 450 455 460
 Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
 465 470 475 480
 Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
 485 490 495
 Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
 500 505 510
 Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
 515 520 525
 Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
 530 535 540
 Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
 545 550 555 560
 Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
 565 570 575
 Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
 580 585 590
 Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
 595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
 610 615 620
 Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
 625 630 640
 Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
 645 650 655
 Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
 660 665 670
 Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
 675 680 685
 Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
 690 695 700
 Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
 705 710 715 720
 Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
 725 730

<210> 219
 <211> 736
 <212> PRT
 <213> vp1, serotype 1

<400> 219

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
 705 710 715 720
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735

<210> 220
 <211> 736
 <212> PRT
 <213> vp1, serotype 6

<400> 220

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525
 Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly

530 535 540
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575
 Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590
 Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
 705 710 715 720
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735

 <210> 221
 <211> 735
 <212> PRT
 <213> vp1, serotype 2

 <400> 221
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg

130					135					140				
Pro Val Glu His Ser	Pro Val Glu Pro Asp Ser	Ser Ser Ser Gly Thr Gly												
145	150	155											160	
Lys Ala Gly Gln Gln	Pro Ala Arg Lys Arg	Leu Asn Phe Gly Gln Thr												
	165	170											175	
Gly Asp Ala Asp	Ser Val Pro Asp Pro	Gln Pro Leu Gly Gln Pro Pro												
180	185	190												
Ala Ala Pro Ser Gly Leu Gly	Thr Asn Thr Met Ala Thr	Gly Ser Gly												
195	200	205												
Ala Pro Met Ala Asp Asn	Asn Glu Gly Ala Asp Gly	Val Gly Asn Ser												
210	215	220												
Ser Gly Asn Trp His	Cys Asp Ser Thr Trp Met	Gly Asp Arg Val Ile												
225	230	235											240	
Thr Thr Ser Thr Arg	Thr Trp Ala Leu Pro	Thr Tyr Asn Asn His											Leu	
	245	250											255	
Tyr Lys Gln Ile Ser Ser Gln Ser	Gly Ala Ser Asn Asp Asn	His Tyr												
	260	265											270	
Phe Gly Tyr Ser Thr Pro Trp	Gly Tyr Phe Asp Phe Asn	Arg Phe His												
275	280	285												
Cys His Phe Ser Pro Arg Asp	Trp Gln Arg Leu Ile Asn Asn Asn Trp													
290	295	300												
Gly Phe Arg Pro Lys Arg	Leu Asn Phe Lys Leu Phe Asn Ile Gln Val													
305	310	315											320	
Lys Glu Val Thr Gln Asn Asp Gly Thr	Thr Thr Ile Ala Asn Asn Leu													
	325	330											335	
Thr Ser Thr Val Gln Val Phe Thr	Asp Ser Glu Tyr Gln Leu Pro Tyr													
	340	345											350	
Val Leu Gly Ser Ala His Gln Gly	Cys Leu Pro Pro Phe Pro Ala Asp													
	355	360											365	
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr	Leu Asn Asn Gly Ser													
	370	375											380	
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys	Leu Glu Tyr Phe Pro Ser													
385	390	395											400	
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr	Phe Ser Tyr Thr Phe Glu													
	405	410											415	
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser	Leu Asp Arg													
	420	425											430	
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr	Leu Ser Arg Thr													
	435	440											445	
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg	Leu Gln Phe Ser Gln													
	450	455											460	
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg	Asn Trp Leu Pro Gly													
	465	470											475	
Pro Cys Tyr Arg Gln Gln Arg Val Ser	Lys Thr Ser Ala Asp Asn Asn													
	485	490											495	

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 222
 <211> 737
 <212> PRT
 <213> vp1, serotype 7
 <400> 222
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
530 535 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
565 570 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 223
<211> 738
<212> PRT
<213> vp1, serotype 8

<400> 223

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
 405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
 450 455 460
 Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
 530 535 540
 Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735
 Asn Leu

<210> 224
 <211> 736
 <212> PRT
 <213> vp1, modified hu.46

<400> 224

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala

355	360	365
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly 370 375 380		
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro 385 390 395 400		
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe 405 410 415		
Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp 420 425 430		
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg 435 440 445		
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser 450 455 460		
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro 465 470 475 480		
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn 485 490 495		
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn 500 505 510		
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys 515 520 525		
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly 530 535 540		
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile 545 550 555 560		
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg 565 570 575		
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala 580 585 590		
Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln 595 600 605		
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His 610 615 620		
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu 625 630 635 640		
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala 645 650 655		
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr 660 665 670		
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln 675 680 685		
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn 690 695 700		
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu 705 710 715 720		

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735

<210> 225
 <211> 735
 <212> PRT
 <213> vp1, modified hu.29
 <400> 225

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 226
<211> 735
<212> PRT
<213> vp1, modified hu.7

<400> 226

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Pro Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
 435 440 445
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
 450 455 460
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
 580 585 590
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 227
<211> 728
<212> PRT
<213> vp1, modified cy.5

<400> 227

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145 150 155 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
 260 265 270
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
 275 280 285
 Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
 290 295 300
 Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
 305 310 315 320
 Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
 325 330 335
 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
 340 345 350
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
 355 360 365
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
 370 375 380
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
 405 410 415
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
 435 440 445
 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
 450 455 460
 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
 465 470 475 480
 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
 485 490 495
 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
 500 505 510
 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
 515 520 525
 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
 530 535 540
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
 545 550 555 560
 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
 580 585 590
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
 595 600 605
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
 Page 345

610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 228
 <211> 728
 <212> PRT
 <213> vp1, modified rh.13

<400> 228

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp

210	215	220
His Cys Asp Ser Thr Trp 225 230	Leu Gly Asp Arg Val 235	Ile Thr Thr Ser Thr 240
Arg Thr Trp Ala Leu 245	Pro Thr Tyr Asn Asn 250	His Leu Tyr Lys Gln Ile 255
Ser Ser Gln Ser Gly Ala Thr Asn 260	Asp Asn His Phe Phe 265	Gly Tyr Ser 270
Thr Pro Trp Gly Tyr Phe Asp 275	Phe Asn Arg Phe His 280	Cys His Phe Ser 285
Pro Arg Asp Trp Gln Arg Leu 290 295	Ile Asn Asn Asn Trp 300	Gly Phe Arg Pro
Arg Lys Leu Arg Phe Lys 305 310	Leu Phe Asn Ile Gln 315	Val Lys Glu Val Thr 320
Thr Asn Asp Gly Val 325	Thr Thr Ile Ala Asn 330	Asn Leu Thr Ser Thr Ile 335
Gln Val Phe Ser 340	Asp Ser Glu Tyr Gln 345	Leu Pro Tyr Val Leu Gly Ser 350
Ala His Gln Gly Cys Leu Pro 355	Pro Phe Pro Ala Asp 360	Val Phe Met Ile 365
Pro Gln Tyr Gly Tyr Leu Thr 370 375	Leu Asn Asn Gly Ser 380	Gln Ser Val Gly
Arg Ser Ser Phe Tyr Cys 385 390	Leu Glu Tyr Phe Pro 395	Ser Gln Met Leu Arg 400
Thr Gly Asn Asn Phe 405	Glu Phe Ser Tyr Thr 410	Phe Glu Glu Val Pro Phe 415
His Ser Ser Tyr Ala His Ser 420	Gln Ser Leu Asp Arg Leu 425	Met Asn Pro 430
Leu Ile Asp Gln Tyr Leu Tyr 435	Tyr Leu Ala Arg Thr 440	Gln Ser Thr Thr 445
Gly Ser Thr Arg Glu Leu 450	Gln Phe His Gln Ala 455	Gly Pro Asn Thr Met 460
Ala Glu Gln Ser Lys Asn 465 470	Trp Leu Pro Gly Pro 475	Cys Tyr Arg Gln Gln 480
Arg Leu Ser Lys Asn 485	Ile Asp Ser Asn Asn 490	Ser Asn Phe Ala Trp 495
Thr Gly Ala Thr Lys Tyr His 500	Leu Asn Gly Arg Asn 505	Ser Leu Thr Asn 510
Pro Gly Val Ala Met Ala Thr 515	Asn Lys Asp Asp Glu 520	Asp Gln Phe Phe 525
Pro Ile Asn Gly Val Leu Val 530 535	Phe Gly Lys Thr Gly 540	Ala Ala Asn Lys
Thr Thr Leu Glu Asn Val 545 550	Leu Met Thr Ser Glu 555	Glu Glu Ile Lys Thr 560
Thr Asn Pro Val Ala 565	Thr Glu Glu Tyr Gly 570	Val Val Ser Ser Asn Leu 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 229
 <211> 729
 <212> PRT
 <213> vp1, modified rh.37

<400> 229

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190
 Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
 195 200 205
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
 260 265 270
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
 275 280 285
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
 290 295 300
 Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
 305 310 315 320
 Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
 325 330 335
 Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
 340 345 350
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
 355 360 365
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
 370 375 380
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
 385 390 395 400
 Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
 405 410 415
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
 420 425 430
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
 435 440 445
 Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
 450 455 460
 Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
 465 470 475 480
 Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
 485 490 495
 Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
 500 505 510
 Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
 515 520 525
 Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
 530 535 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
 545 550 555
 Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
 565 570 575
 Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
 580 585 590
 Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
 595 600 605
 Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
 610 615 620
 Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
 625 630 635 640
 Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
 645 650 655
 Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
 660 665 670
 Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
 675 680 685
 Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
 690 695 700
 Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
 705 710 715 720
 Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725

<210> 230
 <211> 737
 <212> PRT
 <213> vpl, modified rh.67

<400> 230

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 690 695 700
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735

Leu

<210> 231
 <211> 738
 <212> PRT
 <213> vpl, modified rh.2

<400> 231

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu

450 455 460
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
 580 585 590
 Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735
 Asn Leu

<210> 232
 <211> 738
 <212> PRT
 <213> vp1, modified rh.58
 <400> 232

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 233
 <211> 738
 <212> PRT

<213> vpl, modified rh.64

<400> 233

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
 405 410 415
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
 530 535 540
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 234
<211> 735
<212> PRT
<213> vp1, modified ch.5

<400> 234

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
 435 440 445
 Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
 500 505 510
 Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
 580 585 590
 Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln

000

000

670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 235

<211> 736

<212> PRT

<213> vp1, modified rh.8

<400> 235

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn

260 265 270
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
 435 440 445
 Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
 450 455 460
 Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
 485 490 495
 Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
 500 505 510
 Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
 515 520 525
 Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
 530 535 540
 Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
 545 550 555 560
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
 565 570 575
 Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
 580 585 590
 Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
 595 600 605
 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
 705 710 715 720
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 <210> 236
 <211> 737
 <212> PRT
 <213> vp1, modified hu.43
 <400> 236
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
 260 265 270
 His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
 405 410 415
 Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
 435 440 445
 Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
 450 455 460
 Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
 465 470 475 480
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
 485 490 495
 Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
 500 505 510
 Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
 515 520 525
 Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
 530 535 540
 Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
 545 550 555 560
 Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
 565 570 575
 Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
 580 585 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu